

Sequence Listing

<110> Shen Zhen Tsinghua Yuanxing Bio-Pharm Science & Technology Co., Ltd.

<120> Anti-Tumor Molecular Vaccine and Method of making thereof

<130> CGCNS31755

<150> CN02159602.6

<151> 2002-12-27

<160> 27

<170> PatentIn version 3.1

<210> 1

<211> 3633

<212> DNA

<213> ÈÈ(homo sapiens)

<220>

<221> CDS

<222> (1)..(3630)

<223>

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Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
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96

ggc acg agt aac aag ctc acg cag ttg ggc act ttt gaa gat cat ttt

144

260	265	270	
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gcc acc tgc gtg aag aag tgt ccc cgt aat tat gtg gtg aca gat cac Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His 290	295	300	912
ggc tcg tgc gtc cga gcc tgt ggg gcc gac agc tat gag atg gag gaa Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu 305	310	315	960
gac ggc gtc cgc aag tgt aag aag tgc gaa ggg cct tgc cgc aaa gtg Asp Gly Val Arg Lys Cys Lys Cys Glu Gly Pro Cys Arg Lys Val 325	330	335	1008
tgt aac gga ata ggt att ggt gaa ttt aaa gac tca ctc tcc ata aat Cys Asn Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn 340	345	350	1056
gct acg aat att aaa cac ttc aaa aac tgc acc tcc atc agt ggc gat Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp 355	360	365	1104
ctc cac atc ctg ccg gtg gca ttt agg ggt gac tcc ttc aca cat act Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr 370	375	380	1152
cct cct ctg gat cca cag gaa ctg gat att ctg aaa acc gta aag gaa Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu 385	390	395	1200
atc aca ggg ttt ttg ctg att cag gct tgg cct gaa aac agg acg gac Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp 405	410	415	1248
ctc cat gcc ttt gag aac cta gaa atc ata cgc ggc agg acc aag caa Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln 420	425	430	1296
cat ggt cag ttt tct ctt gca gtc gtc agc ctg aac ata aca tcc ttg His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu 435	440	445	1344
gga tta cgc tcc ctc aag gag ata agt gat gga gat gtg ata att tca Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser 450	455	460	1392
gga aac aaa aat ttg tgc tat gca aat aca ata aac tgg aaa aaa ctg Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu 465	470	475	1440
ttt ggg acc tcc ggt cag aaa acc aaa att ata agc aac aga ggt gaa Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu 485	490	495	1488

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515 520 525	
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565 570 575	
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580 585 590	
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595 600 605	
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610 615 620	
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625 630 635 640	
cct aag atc ccg tcc atc gcc act ggg atg gtg ggg gcc ctc ctc ttg Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu	1968
645 650 655	
ctg ctg gtg gtc ctg ggg atc ggc ctc ttc atg cga agg cg ^g cac Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His	2016
660 665 670	
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675 680 685	
gtg gag cct ctt aca ccc agt gga gaa gct ccc aac caa gct ctc ttg Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu	2112
690 695 700	
agg atc ttg aag gaa act gaa ttc aaa aag atc aaa gtg ctg ggc tcc Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser	2160
705 710 715 720	

ggt gcg ttc ggc acg gtg tat aag gga ctc tgg atc cca gaa ggt gag Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu 725 730 735	2208
aaa gtt aaa att ccc gtc gct atc aag gaa tta aga gaa gca aca tct Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser 740 745 750	2256
ccg aaa gcc aac aag gaa atc ctc gat gaa gcc tac gtg atg gcc agc Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser 755 760 765	2304
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acc gtg cag ctc atc acg cag ctc atg ccc ttc ggc tgc ctc ctg gac Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp 785 790 795 800	2400
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gaa gag aaa gaa tac cat gca gaa gga ggc aaa gtg cct atc aag tgg Glu Glu Lys Glu Tyr His Ala Glu Gly Lys Val Pro Ile Lys Trp 865 870 875 880	2640
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Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys			
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Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln			
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cgc tac ctt gtc att cag ggg gat gaa aga atg cat ttg cca agt cct			2976
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980	985	990	
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Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp			
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Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe			
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Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu			
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Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn			
1040	1045	1050	
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Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg			
1055	1060	1065	
tac agc tca gac ccc aca ggc gcc ttg act gag gac agc ata gac			3249
Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp			
1070	1075	1080	
gac acc ttc ctc cca gtg cct gaa tac ata aac cag tcc gtt ccc			3294
Asp Thr Phe Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val Pro			
1085	1090	1095	
aaa agg ccc gct ggc tct gtg cag aat cct gtc tat cac aat cag			3339
Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln			
1100	1105	1110	
cct ctg aac ccc gcg ccc agc aga gac cca cac tac cag gac ccc			3384
Pro Leu Asn Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro			
1115	1120	1125	
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His Ser Thr Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Val Gln			
1130	1135	1140	
ccc acc tgt gtc aac agc aca ttc gac agc cct gcc cac tgg gcc			3474
Pro Thr Cys Val Asn Ser Thr Phe Asp Ser Pro Ala His Trp Ala			
1145	1150	1155	
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Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp Tyr Gln			

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Gln Asp Phe Phe Pro Lys Glu	Ala Lys Pro Asn Gly	Ile Phe Lys	
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ggc tcc aca gct gaa aat gca	gaa tac cta agg gtc	gcg cca caa	3609
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Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe			
35	40	45	
Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn			
50	55	60	
Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys			
65	70	75	80
Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val			
85	90	95	
Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr			
100	105	110	
Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn			
115	120	125	

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
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His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

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245 250 255

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Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

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Asp Gly Val Arg Lys Cys Lys Cys Glu Gly Pro Cys Arg Lys Val
325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
340 345 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
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Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
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His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
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Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
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Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
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545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
645 650 655

Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
660 665 670

Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
675 680 685

Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
690 695 700

Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
705 710 715 720

Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
725 730 735

Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
740 745 750

Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
755 760 765

Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
770 775 780

Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
785 790 795 800

Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn

805

810

815

Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
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Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
835 840 845

Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
850 855 860

Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
865 870 875 880

Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
885 890 895

Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
900 905 910

Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
915 920 925

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
930 935 940

Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
945 950 955 960

Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
965 970 975

Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
980 985 990

Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp
995 1000 1005

Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe
1010 1015 1020

Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu
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Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg
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Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp
1070 1075 1080

Asp Thr Phe Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val Pro
1085 1090 1095

Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln
1100 1105 1110

Pro Leu Asn Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro
1115 1120 1125

His Ser Thr Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Val Gln
1130 1135 1140

Pro Thr Cys Val Asn Ser Thr Phe Asp Ser Pro Ala His Trp Ala
1145 1150 1155

Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp Tyr Gln
1160 1165 1170

Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn Gly Ile Phe Lys
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Ser Ser Glu Phe Ile Gly Ala
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<212> DNA

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<222> (1)..(1971)

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Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

ggc acg agt aac aag ctc acg cag ttg ggc act ttt gaa gat cat ttt 144
Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

ctc agc ctc cag agg atg ttc aat aac tgt gag gtg gtc ctt ggg aat 192
Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
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Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65 70 75 80

acc atc cag gag gtg gct ggt tat gtc ctc att gcc ctc aac aca gtg 288
Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

gag cga att cct ttg gaa aac ctg cag atc atc aga gga aat atg tac 336
Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

tac gaa aat tcc tat gcc tta gca gtc tta tct aac tat gat gca aat 384
Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

aaa acc gga ctg aag gag ctg ccc atg aga aat tta cag gaa atc ctg 432
Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

cat ggc gcc gtg cgg ttc agc aac aac cct gcc ctg tgc aac gtg gag 480
His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

agc atc cag tgg cgg gac ata gtc agt gac ttt ctc agc aac atg 528
Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

tcg atg gac ttc cag aac cac ctg ggc agc tgc caa aag tgt gat cca		576	
Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro			
180	185	190	
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Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Asn Cys Gln			
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Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg			
210	215	220	
ggc aag tcc ccc agt gac tgc tgc cac aac cag tgt gct gca ggc tgc		720	
Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys			
225	230	235	240
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Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp			
245	250	255	
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Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro			
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Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly			
275	280	285	
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Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His			
290	295	300	
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Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu			
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Asp Gly Val Arg Lys Cys Lys Cys Glu Gly Pro Cys Arg Lys Val			
325	330	335	
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Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn			
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Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp			
355	360	365	
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Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr			
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Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu			
385	390	395	400

atc aca ggg ttt ttg ctg att cag gct tgg cct gaa aac agg acg gac Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp 405 410 415	1248
ctc cat gcc ttt gag aac cta gaa atc ata cgc ggc agg acc aag caa Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln 420 425 430	1296
cat ggt cag ttt tct ctt gca gtc gtc agc ctg aac ata aca tcc ttg His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu 435 440 445	1344
gga tta cgc tcc ctc aag gag ata agt gat gga gat gtg ata att tca Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser 450 455 460	1392
gga aac aaa aat ttg tgc tat gca aat aca ata aac tgg aaa aaa ctg Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu 465 470 475 480	1440
ttt ggg acc tcc ggt cag aaa acc aaa att ata agc aac aga ggt gaa Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu 485 490 495	1488
aac agc tgc aag gcc aca ggc cag gtc tgc cat gcc ttg tgc tcc ccc Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro 500 505 510	1536
gag ggc tgc tgg ggc ccg gag ccc agg gac tgc gtc tct tgc cgg aat Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn 515 520 525	1584
gtc agc cga ggc agg gaa tgc gtg gac aag tgc aac ctt ctg gag ggt Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly 530 535 540	1632
gag cca agg gag ttt gtg gag aac tct gag tgc ata cag tgc cac cca Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro 545 550 555 560	1680
gag tgc ctg cct cag gcc atg aac atc acc tgc aca gga cgg gga cca Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro 565 570 575	1728
gac aac tgt atc cag tgt gcc cac tac att gac ggc ccc cac tgc gtc Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val 580 585 590	1776
aag acc tgc ccg gca gga gtc atg gga gaa aac aac acc ctg gtc tgg Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp 595 600 605	1824
aag tac gca gac gcc ggc cat gtg tgc cac ctg tgc cat cca aac tgc Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys 610 615 620	1872
acc tac gga tgc act ggg cca ggt ctt gaa ggc tgt cca acg aat gga	1920

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

agc tac ata gtg tct cac ttt cca aga tca ttc tac aag atg tca gtg 1968
Ser Tyr Ile Val Ser His Phe Pro Arg Ser Phe Tyr Lys Met Ser Val
645 650 655

cac tga 1974
His

<210> 4

<211> 657

<212> PRT

<213> Human homo sapiens)

<400> 4

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Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65 70 75 80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu

130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305 310 315 320

Asp Gly Val Arg Lys Cys Lys Cys Glu Gly Pro Cys Arg Lys Val
325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
340 345 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

Ser Tyr Ile Val Ser His Phe Pro Arg Ser Phe Tyr Lys Met Ser Val
645 650 655

His

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<211> 2118

<212> DNA

<213> Human(homo sapiens)

<220>

<221> CDS

<222> (1)..(2115)

<223>

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Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Ala
1 5 10 15

gcg ctc tgc ccg gcg agt cggt gct ctg gag gaa aag aaa gtt tgc caa 96
Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

ggc acg agt aac aag ctc acg cag ttg ggc act ttt gaa gat cat ttt 144
Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

ctc agc ctc cag agg atg ttc aat aac tgt gag gtg gtc ctt ggg aat 192
Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

ttg gaa att acc tat gtg cag agg aat tat gat ctt tcc ttc tta aag Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys 65 70 75 80	240
acc atc cag gag gtg gct ggt tat gtc ctc att gcc ctc aac aca gtg Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val 85 90 95	288
gag cga att cct ttg gaa aac ctg cag atc atc aga gga aat atg tac Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr 100 105 110	336
tac gaa aat tcc tat gcc tta gca gtc tta tct aac tat gat gca aat Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn 115 120 125	384
aaa acc gga ctg aag gag ctg ccc atg aga aat tta cag gaa atc ctg Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu 130 135 140	432
cat ggc gcc gtg cgg ttc agc aac aac cct gcc ctg tgc aac gtg gag His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu 145 150 155 160	480
agc atc cag tgg cgg gac ata gtc agc agt gac ttt ctc agc aac atg Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met 165 170 175	528
tcg atg gac ttc cag aac cac ctg ggc agc tgc caa aag tgt gat cca Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro 180 185 190	576
agc tgt ccc aat ggg agc tgc tgg ggt gca gga gag gag aac tgc cag Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Asn Cys Gln 195 200 205	624
aaa ctg acc aaa atc atc tgt gcc cag tgc tcc ggg cgc tgc cgt Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg 210 215 220	672
ggc aag tcc ccc agt gac tgc tgc cac aac cag tgt gct gca ggc tgc Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys 225 230 235 240	720
aca ggc ccc cgg gag agc gac tgc ctg gtc tgc cgc aaa ttc cga gac Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp 245 250 255	768
gaa gcc acg tgc aag gac acc tgc ccc cca ctc atg ctc tac aac ccc Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro 260 265 270	816
acc acg tac cag atg gat gtg aac ccc gag ggc aaa tac agc ttt ggt Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly 275 280 285	864

gcc acc tgc gtg aag aag tgt ccc cgt aat tat gtg gtg aca gat cac Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His 290 295 300	912
ggc tcg tgc gtc cga gcc tgt ggg gcc gac agc tat gag atg gag gaa Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu 305 310 315 320	960
gac ggc gtc cgc aag tgt aag aag tgc gaa ggg cct tgc cgc aaa gtg Asp Gly Val Arg Lys Cys Lys Cys Glu Gly Pro Cys Arg Lys Val 325 330 335	1008
tgt aac gga ata ggt att ggt gaa ttt aaa gac tca ctc tcc ata aat Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn 340 345 350	1056
gct acg aat att aaa cac ttc aaa aac tgc acc tcc atc agt ggc gat Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp 355 360 365	1104
ctc cac atc ctg ccg gtg gca ttt agg ggt gac tcc ttc aca cat act Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr 370 375 380	1152
cct cct ctg gat cca cag gaa ctg gat att ctg aaa acc gta aag gaa Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu 385 390 395 400	1200
atc aca ggg ttt ttg ctg att cag gct tgg cct gaa aac agg acg gac Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp 405 410 415	1248
ctc cat gcc ttt gag aac cta gaa atc ata cgc ggc agg acc aag caa Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln 420 425 430	1296
cat ggt cag ttt tct ctt gca gtc gtc agc ctg aac ata aca tcc ttg His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu 435 440 445	1344
gga tta cgc tcc ctc aag gag ata agt gat gga gat gtg ata att tca Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser 450 455 460	1392
gga aac aaa aat ttg tgc tat gca aat aca ata aac tgg aaa aaa ctg Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu 465 470 475 480	1440
ttt ggg acc tcc ggt cag aaa acc aaa att ata agc aac aga ggt gaa Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu 485 490 495	1488
aac agc tgc aag gcc aca ggc cag gtc tgc cat gcc ttg tgc tcc ccc Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro 500 505 510	1536
gag ggc tgc tgg ggc ccg gag ccc agg gac tgc gtc tct tgc cg aat	1584

Glu	Gly	Cys	Trp	Gly	Pro	Glu	Pro	Arg	Asp	Cys	Val	Ser	Cys	Arg	Asn		
515						520						525					
gtc agc cga ggc agg gaa tgc gtg gac aag tgc aac ctt ctg gag ggt															1632		
Val	Ser	Arg	Gly	Arg	Glu	Cys	Val	Asp	Lys	Cys	Asn	Leu	Leu	Glu	Gly		
530						535						540					
gag cca agg gag ttt gtg gag aac tct gag tgc ata cag tgc cac cca															1680		
Glu	Pro	Arg	Glu	Phe	Val	Glu	Asn	Ser	Glu	Cys	Ile	Gln	Cys	His	Pro		
545						550					555				560		
gag tgc ctg cct cag gcc atg aac atc acc tgc aca gga cgg gga cca															1728		
Glu	Cys	Leu	Pro	Gln	Ala	Met	Asn	Ile	Thr	Cys	Thr	Gly	Arg	Gly	Pro		
565						570					575						
gac aac tgt atc cag tgt gcc cac tac att gac ggc ccc cac tgc gtc															1776		
Asp	Asn	Cys	Ile	Gln	Ala	His	Tyr	Ile	Asp	Gly	Pro	His	Cys	Val			
580						585					590						
aag acc tgc ccg gca gga gtc atg gga gaa aac aac acc ctg gtc tgg															1824		
Lys	Thr	Cys	Pro	Ala	Gly	Val	Met	Gly	Glu	Asn	Asn	Thr	Leu	Val	Trp		
595						600					605						
aag tac gca gac gcc ggc cat gtg tgc cac ctg tgc cat cca aac tgc															1872		
Lys	Tyr	Ala	Asp	Ala	Gly	His	Val	Cys	His	Leu	Cys	His	Pro	Asn	Cys		
610						615					620						
acc tac ggg cca gga aat gag agt ctc aaa gcc atg tta ttc tgc ctt															1920		
Thr	Tyr	Gly	Pro	Gly	Asn	Glu	Ser	Leu	Lys	Ala	Met	Leu	Phe	Cys	Leu		
625						630					635				640		
ttt aaa cta tca tcc tgt aat caa agt aat gat ggc agc gtg tcc cac															1968		
Phe	Lys	Leu	Ser	Ser	Cys	Asn	Gln	Ser	Asn	Asp	Gly	Ser	Val	Ser	His		
645						645					650			655			
cag agc ggg agc cca gct gct cag gag tca tgc tta gga tgg atc cct															2016		
Gln	Ser	Gly	Ser	Pro	Ala	Ala	Gln	Glu	Ser	Cys	Leu	Gly	Trp	Ile	Pro		
660						660					665			670			
tct ctt ctg ccg tca gag ttt cag ctg ggt tgg ggt gga tgc agc cac															2064		
Ser	Leu	Leu	Pro	Ser	Glu	Phe	Gln	Leu	Gly	Trp	Gly	Gly	Cys	Ser	His		
675						680					685						
ctc cat gcc tgg cct tct gca tct gtg atc atc acg gcc tcc tcc tgc															2112		
Leu	His	Ala	Trp	Pro	Ser	Ala	Ser	Val	Ile	Ile	Thr	Ala	Ser	Ser	Cys		
690						695					700						
cac	tga															2118	
His																	
705																	

<210> 6

<211> 705

<212> PRT

<213> Human(homo sapiens)

<400> 6

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20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65 70 75 80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305 310 315 320

Asp Gly Val Arg Lys Cys Lys Cys Glu Gly Pro Cys Arg Lys Val
325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
340 345 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Pro Gly Asn Glu Ser Leu Lys Ala Met Leu Phe Cys Leu
625 630 635 640

Phe Lys Leu Ser Ser Cys Asn Gln Ser Asn Asp Gly Ser Val Ser His
645 650 655

Gln Ser Gly Ser Pro Ala Ala Gln Glu Ser Cys Leu Gly Trp Ile Pro
660 665 670

Ser Leu Leu Pro Ser Glu Phe Gln Leu Gly Trp Gly Gly Cys Ser His
675 680 685

Leu His Ala Trp Pro Ser Ala Ser Val Ile Ile Thr Ala Ser Ser Cys
690 695 700

His
705

<210> 7

<211> 1887

<212> DNA

<213> Human homo sapiens)

<220>

<221> CDS

<222> (1)..(1884)

<223>

<400> 7

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gcg ctc tgc ccg gcg agt cggt gct ctg gag gaa aag aaa gtt tgc caa 96
Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

ggc acg agt aac aag ctc acg cag ttg ggc act ttt gaa gat cat ttt 144
Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

ctc agc ctc cag agg atg ttc aat aac tgt gag gtg gtc ctt ggg aat 192
Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

ttg gaa att acc tat gtg cag agg aat tat gat ctt tcc ttc tta aag 240
Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65 70 75 80

acc atc cag gag gtg gct ggt tat gtc ctc att gcc ctc aac aca gtg		288	
Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val			
85	90	95	
gag cga att cct ttg gaa aac ctg cag atc atc aga gga aat atg tac		336	
Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr			
100	105	110	
tac gaa aat tcc tat gcc tta gca gtc tta tct aac tat gat gca aat		384	
Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn			
115	120	125	
aaa acc gga ctg aag gag ctg ccc atg aga aat tta cag gaa atc ctg		432	
Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu			
130	135	140	
cat ggc gcc gtg cgg ttc agc aac aac cct gcc ctg tgc aac gtg gag		480	
His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu			
145	150	155	160
agc atc cag tgg cgg gac ata gtc agc agt gac ttt ctc agc aac atg		528	
Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met			
165	170	175	
tcg atg gac ttc cag aac cac ctg ggc agc tgc caa aag tgt gat cca		576	
Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro			
180	185	190	
agc tgt ccc aat ggg agc tgc tgg ggt gca gga gag gag aac tgc cag		624	
Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln			
195	200	205	
aaa ctg acc aaa atc atc tgt gcc cag cag tgc tcc ggg cgc tgc cgt		672	
Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg			
210	215	220	
ggc aag tcc ccc agt gac tgc tgc cac aac cag tgt gct gca ggc tgc		720	
Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys			
225	230	235	240
aca ggc ccc cgg gag agc gac tgc ctg gtc tgc cgc aaa ttc cga gac		768	
Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp			
245	250	255	
gaa gcc acg tgc aag gac acc tgc ccc cca ctc atg ctc tac aac ccc		816	
Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro			
260	265	270	
acc acg tac cag atg gat gtg aac ccc gag ggc aaa tac agc ttt ggt		864	
Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly			
275	280	285	
gcc acc tgc gtg aag aag tgt ccc cgt aat tat gtg gtg aca gat cac		912	
Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His			
290	295	300	
ggc tcg tgc gtc cga gcc tgt ggg gcc gac agc tat gag atg gag gaa		960	

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu			
305	310	315	320
gac ggc gtc cgc aag tgt aag aag tgc gaa ggg cct tgc cgc aaa gtg			1008
Asp Gly Val Arg Lys Cys Lys Cys Glu Gly Pro Cys Arg Lys Val			
325	330	335	
tgt aac gga ata ggt att ggt gaa ttt aaa gac tca ctc tcc ata aat			1056
Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn			
340	345	350	
gct acg aat att aaa cac ttc aaa aac tgc acc tcc atc agt ggc gat			1104
Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp			
355	360	365	
ctc cac atc ctg ccg gtg gca ttt agg ggt gac tcc ttc aca cat act			1152
Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr			
370	375	380	
cct cct ctg gat cca cag gaa ctg gat att ctg aaa acc gta aag gaa			1200
Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu			
385	390	395	400
atc aca ggg ttt ttg ctg att cag gct tgg cct gaa aac agg acg gac			1248
Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp			
405	410	415	
ctc cat gcc ttt gag aac cta gaa atc ata cgc ggc agg acc aag caa			1296
Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln			
420	425	430	
cat ggt cag ttt tct ctt gca gtc gtc agc ctg aac ata aca tcc ttg			1344
His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu			
435	440	445	
gga tta cgc tcc ctc aag gag ata agt gat gga gat gtg ata att tca			1392
Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser			
450	455	460	
gga aac aaa aat ttg tgc tat gca aat aca ata aac tgg aaa aaa ctg			1440
Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu			
465	470	475	480
ttt ggg acc tcc ggt cag aaa acc aaa att ata agc aac aga ggt gaa			1488
Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu			
485	490	495	
aac agc tgc aag gcc aca ggc cag gtc tgc cat gcc ttg tgc tcc ccc			1536
Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro			
500	505	510	
gag ggc tgc tgg ggc ccg gag ccc agg gac tgc gtc tct tgc cgg aat			1584
Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn			
515	520	525	
gtc agc cga ggc agg gaa tgc gtg gac aag tgc aac ctt ctg gag ggt			1632
Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly			

530	535	540	
gag cca agg gag ttt gtg gag aac tct gag tgc ata cag tgc cac cca Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro			1680
545	550	555	560
gag tgc ctg cct cag gcc atg aac atc acc tgc aca gga cgg gga cca Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro			1728
	565	570	575
gac aac tgt atc cag tgt gcc cac tac att gac ggc ccc cac tgc gtc Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val			1776
580	585	590	
aag acc tgc ccg gca gga gtc atg gga gaa aac aac acc ctg gtc tgg Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp			1824
595	600	605	
aag tac gca gac gcc ggc cat gtg tgc cac ctg tgc cat cca aac tgc Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys			1872
610	615	620	
acc tac ggg tcc taa Thr Tyr Gly Ser			1887
625			
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<211> 628			
<212> PRT			
<213> Human(homo sapiens)			
<400> 8			
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1	5	10	15
Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln			
20	25	30	
Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe			
35	40	45	
Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn			
50	55	60	
Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys			
65	70	75	80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305 310 315 320

Asp Gly Val Arg Lys Cys Lys Cys Glu Gly Pro Cys Arg Lys Val
325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
340 345 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Ser
625

<210> 9

<211> 1218

<212> DNA

<213> Human homo sapiens)

<220>

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<222> (1)..(1215)

<223>

<400> 9
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Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

gcg ctc tgc ccg gcg agt cggt gct ctg gag gaa aag aaa gtt tgc caa 96
Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

ggc acg agt aac aag ctc acg cag ttg ggc act ttt gaa gat cat ttt		144	
Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe			
35	40	45	
ctc agc ctc cag agg atg ttc aat aac tgt gag gtg gtc ctt ggg aat		192	
Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn			
50	55	60	
ttg gaa att acc tat gtg cag agg aat tat gat ctt tcc ttc tta aag		240	
Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys			
65	70	75	80
acc atc cag gag gtg gct ggt tat gtc ctc att gcc ctc aac aca gtg		288	
Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val			
85	90	95	
gag cga att cct ttg gaa aac ctg cag atc atc aga gga aat atg tac		336	
Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr			
100	105	110	
tac gaa aat tcc tat gcc tta gca gtc tta tct aac tat gat gca aat		384	
Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn			
115	120	125	
aaa acc gga ctg aag gag ctg ccc atg aga aat tta cag gaa atc ctg		432	
Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu			
130	135	140	
cat ggc gcc gtg cgg ttc agc aac aac cct gcc ctg tgc aac gtg gag		480	
His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu			
145	150	155	160
agc atc cag tgg cgg gac ata gtc agc agt gac ttt ctc agc aac atg		528	
Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met			
165	170	175	
tcg atg gac ttc cag aac cac ctg ggc agc tgc caa aag tgt gat cca		576	
Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro			
180	185	190	
agc tgt ccc aat ggg agc tgc tgg ggt gca gga gag gag aac tgc cag		624	
Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln			
195	200	205	
aaa ctg acc aaa atc atc tgt gcc cag cag tgc tcc ggg cgc tgc cgt		672	
Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg			
210	215	220	
ggc aag tcc ccc agt gac tgc tgc cac aac cag tgt gct gca ggc tgc		720	
Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys			
225	230	235	240
aca ggc ccc cgg gag agc gac tgc ctg gtc tgc cgc aaa ttc cga gac		768	
Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp			
245	250	255	
gaa gcc acg tgc aag gac acc tgc ccc cca ctc atg ctc tac aac ccc		816	

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro			
260	265	270	
acc acg tac cag atg gat gtg aac ccc gag ggc aaa tac agc ttt ggt			864
Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly			
275	280	285	
gcc acc tgc gtg aag aag tgt ccc cgt aat tat gtg gtg aca gat cac			912
Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His			
290	295	300	
ggc tcg tgc gtc cga gcc tgt ggg gcc gac agc tat gag atg gag gaa			960
Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu			
305	310	315	320
gac ggc gtc cgc aag tgt aag aag tgc gaa ggg cct tgc cgc aaa gtg			1008
Asp Gly Val Arg Lys Cys Lys Cys Glu Gly Pro Cys Arg Lys Val			
325	330	335	
tgt aac gga ata ggt att ggt gaa ttt aaa gac tca ctc tcc ata aat			1056
Cys Asn Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn			
340	345	350	
gct acg aat att aaa cac ttc aaa aac tgc acc tcc atc agt ggc gat			1104
Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp			
355	360	365	
ctc cac atc ctg ccg gtg gca ttt agg ggt gac tcc ttc aca cat act			1152
Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr			
370	375	380	
cct cct ctg gat cca cag gaa ctg gat att ctg aaa acc gta aag gaa			1200
Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu			
385	390	395	400
atc aca ggt ttg agc tga			1218
Ile Thr Gly Leu Ser			
405			

<210> 10

<211> 405

<212> PRT

<213> Human (homo sapiens)

<400> 10

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20

25

30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65 70 75 80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305 310 315 320

Asp Gly Val Arg Lys Cys Lys Cys Glu Gly Pro Cys Arg Lys Val
325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
340 345 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Leu Ser
405

<210> 11

<211> 2829

<212> DNA

<213> ÈÈ(homo sapiens)

<220>

<221> CDS

<222> (1)...(2826)

<223>

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Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala			
1 5 10 15			
gcg ctc tgc ccg gcg agt cggt gct ctg gag gaa aag cgt aat tat gtg			96
Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Arg Asn Tyr Val			
20 25 30			
gtg aca gat cac ggc tcg tgc cga gcc tgt ggg gcc gac agc tat			144
Val Thr Asp His Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr			
35 40 45			
gag atg gag gaa gac ggc gtc cgc aag tgt aag aag tgc gaa ggg cct			192
Glu Met Glu Glu Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro			
50 55 60			
tgc cgc aaa gtg tgt aac gga ata ggt att ggt gaa ttt aaa gac tca			240
Cys Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser			
65 70 75 80			
ctc tcc ata aat gct acg aat att aaa cac ttc aaa aac tgc acc tcc			288
Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser			
85 90 95			
atc agt ggc gat ctc cac atc ctg ccg gtg gca ttt agg ggt gac tcc			336
Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser			
100 105 110			
ttc aca cat act cct ctg gat cca cag gaa ctg gat att ctg aaa			384
Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys			
115 120 125			
acc gta aag gaa atc aca ggg ttt ttg ctg att cag gct tgg cct gaa			432
Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu			
130 135 140			
aac agg acg gac ctc cat gcc ttt gag aac cta gaa atc ata cgc ggc			480
Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly			
145 150 155 160			
agg acc aag caa cat ggt cag ttt tct ctt gca gtc gtc agc ctg aac			528
Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn			
165 170 175			
ata aca tcc ttg gga tta cgc tcc ctc aag gag ata agt gat gga gat			576
Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp			
180 185 190			
gtg ata att tca gga aac aaa aat ttg tgc tat gca aat aca ata aac			624
Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn			
195 200 205			

tgg aaa aaa ctg ttt ggg acc tcc ggt cag aaa acc aaa att ata agc Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser	210	215	220	672
aac aga ggt gaa aac aac tgc aag gcc aca ggc cag gtc tgc cat gcc Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala	225	230	235	240
ttg tgc tcc ccc gag ggc tgc tgg ggc ccg gag ccc agg gac tgc gtc Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val	245	250	255	768
tct tgc cgg aat gtc agc cga ggc agg gaa tgc gtg gac aag tgc aac Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn	260	265	270	816
ctt ctg gag ggt gag cca agg gag ttt gtg gag aac tct gag tgc ata Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile	275	280	285	864
cag tgc cac cca gag tgc ctg cct cag gcc atg aac atc acc tgc aca Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr	290	295	300	912
gga cgg gga cca gac aac tgt atc cag tgt gcc cac tac att gac ggc Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly	305	310	315	960
ccc cac tgc gtc aag acc tgc ccg gca gga gtc atg gga gaa aac aac Pro His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn	325	330	335	1008
acc ctg gtc tgg aag tac gca gac gcc ggc cat gtg tgc cac ctg tgc Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys	340	345	350	1056
cat cca aac tgc acc tac gga tgc act ggg cca ggt ctt gaa ggc tgt His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys	355	360	365	1104
cca acg aat ggg cct aag atc ccg tcc atc gcc act ggg atg gtg ggg Pro Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly	370	375	380	1152
gcc ctc ctc ttg ctg ctg gtg gtg gcc ctg ggg atc ggc ctc ttc atg Ala Leu Leu Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met	385	390	395	1200
cga agg cgc cac atc gtt cgg aag cgc acg ctg cgg agg ctg ctg cag Arg Arg Arg His Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln	405	410	415	1248
gag agg gag ctt gtg gag cct ctt aca ccc agt gga gaa gct ccc aac Glu Arg Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn	420	425	430	1296

caa gct ctc ttg agg atc ttg aag gaa act gaa ttc aaa aag atc aaa Gln Ala Leu Leu Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys 435 440 445	1344
gtg ctg ggc tcc ggt gcg ttc ggc acg gtg tat aag gga ctc tgg atc Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile 450 455 460	1392
cca gaa ggt gag aaa gtt aaa att ccc gtc gct atc aag gaa tta aga Pro Glu Gly Glu Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg 465 470 475 480	1440
gaa gca aca tct ccg aaa gcc aac aag gaa atc ctc gat gaa gcc tac Glu Ala Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr 485 490 495	1488
gtg atg gcc agc gtg gac aac ccc cac gtg tgc cgc ctg ctg ggc atc Val Met Ala Ser Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile 500 505 510	1536
tgc ctc acc tcc acc gtg cag ctc atc acg cag ctc atg ccc ttc ggc Cys Leu Thr Ser Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly 515 520 525	1584
tgc ctc ctg gac tat gtc cgg gaa cac aaa gac aat att ggc tcc cag Cys Leu Leu Asp Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln 530 535 540	1632
tac ctg ctc aac tgg tgt gtg cag atc gca aag ggc atg aac tac ttg Tyr Leu Leu Asn Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu 545 550 555 560	1680
gag gac cgt cgc ttg gtg cac cgc gac ctg gca gcc agg aac gta ctg Glu Asp Arg Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu 565 570 575	1728
gtg aaa aca ccg cag cat gtc aag atc aca gat ttt ggg ctg gcc aaa Val Lys Thr Pro Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys 580 585 590	1776
ctg ctg ggt gcg gaa gag aaa gaa tac cat gca gaa gga ggc aaa gtg Leu Leu Gly Ala Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val 595 600 605	1824
cct atc aag tgg atg gca ttg gaa tca att tta cac aga atc tat acc Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr 610 615 620	1872
cac cag agt gat gtc tgg agc tac ggg gtg acc gtt tgg gag ttg atg His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met 625 630 635 640	1920
acc ttt gga tcc aag cca tat gac gga atc cct gcc agc gag atc tcc Thr Phe Gly Ser Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser 645 650 655	1968
tcc atc ctg gag aaa gga gaa cgc ctc cct cag cca ccc ata tgt acc	2016

Ser Ile Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr			
660	665	670	
atc gat gtc tac atg atc atg gtc aag tgc tgg atg ata gac gca gat			2064
Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp			
675	680	685	
agt cgc cca aag ttc cgt gag ttg atc atc gaa ttc tcc aaa atg gcc			2112
Ser Arg Pro Lys Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala			
690	695	700	
cga gac ccc cag cgc tac ctt gtc att cag ggg gat gaa aga atg cat			2160
Arg Asp Pro Gln Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His			
705	710	715	720
ttg cca agt cct aca gac tcc aac ttc tac cgt gcc ctg atg gat gaa			2208
Leu Pro Ser Pro Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu			
725	730	735	
gaa gac atg gac gac gtg gtg gat gcc gac gag tac ctc atc cca cag			2256
Glu Asp Met Asp Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln			
740	745	750	
cag ggc ttc ttc agc agc ccc tcc acg tca cgg act ccc ctc ctg agc			2304
Gln Gly Phe Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser			
755	760	765	
tct ctg agt gca acc agc aac aat tcc acc gtg gct tgc att gat aga			2352
Ser Leu Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg			
770	775	780	
aat ggg ctg caa agc tgt ccc atc aag gaa gac agc ttc ttg cag cga			2400
Asn Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg			
785	790	795	800
tac agc tca gac ccc aca ggc gcc ttg act gag gac agc ata gac gac			2448
Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp Asp			
805	810	815	
acc ttc ctc cca gtg cct gaa tac ata aac cag tcc gtt ccc aaa agg			2496
Thr Phe Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val Pro Lys Arg			
820	825	830	
ccc gct ggc tct gtg cag aat cct gtc tat cac aat cag cct ctg aac			2544
Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln Pro Leu Asn			
835	840	845	
ccc gcg ccc agc aga gac cca cac tac cag gac ccc cac agc act gca			2592
Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro His Ser Thr Ala			
850	855	860	
gtg ggc aac ccc gag tat ctc aac act gtc cag ccc acc tgt gtc aac			2640
Val Gly Asn Pro Glu Tyr Leu Asn Thr Val Gln Pro Thr Cys Val Asn			
865	870	875	880
agc aca ttc gac agc cct gcc cac tgg gcc cag aaa ggc agc cac caa			2688
Ser Thr Phe Asp Ser Pro Ala His Trp Ala Gln Lys Gly Ser His Gln			

885	890	895	
att agc ctg gac aac cct gac tac cag cag gac ttc ttt ccc aag gaa Ile Ser Leu Asp Asn Pro Asp Tyr Gln Gln Asp Phe Phe Pro Lys Glu 900 905 910			2736
gcc aag cca aat ggc atc ttt aag ggc tcc aca gct gaa aat gca gaa Ala Lys Pro Asn Gly Ile Phe Lys Gly Ser Thr Ala Glu Asn Ala Glu 915 920 925			2784
tac cta agg gtc gcg cca caa agc agt gaa ttt att gga gca tga Tyr Leu Arg Val Ala Pro Gln Ser Ser Glu Phe Ile Gly Ala 930 935 940			2829
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Glu Met Glu Glu Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro 50 55 60			
Cys Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser 65 70 75 80			
Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser 85 90 95			
Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser 100 105 110			
Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys 115 120 125			

Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu
130 135 140

Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly
145 150 155 160

Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn
165 170 175

Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp
180 185 190

Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn
195 200 205

Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser
210 215 220

Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala
225 230 235 240

Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val
245 250 255

Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn
260 265 270

Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile
275 280 285

Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr
290 295 300

Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly
305 310 315 320

Pro His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn
325 330 335

Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys
340 345 350

His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys
355 360 365

Pro Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly
370 375 380

Ala Leu Leu Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met
385 390 395 400

Arg Arg Arg His Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln
405 410 415

Glu Arg Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn
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Gln Ala Leu Leu Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys
435 440 445

Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile
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Pro Glu Gly Glu Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg
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Glu Ala Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr
485 490 495

Val Met Ala Ser Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile
500 505 510

Cys Leu Thr Ser Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly
515 520 525

Cys Leu Leu Asp Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln
530 535 540

Tyr Leu Leu Asn Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu
545 550 555 560

Glu Asp Arg Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu
565 570 575

Val Lys Thr Pro Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys
580 585 590

Leu Leu Gly Ala Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val
595 600 605

Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr
610 615 620

His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met
625 630 635 640

Thr Phe Gly Ser Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser
645 650 655

Ser Ile Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr
660 665 670

Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp
675 680 685

Ser Arg Pro Lys Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala
690 695 700

Arg Asp Pro Gln Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His
705 710 715 720

Leu Pro Ser Pro Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu
725 730 735

Glu Asp Met Asp Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln
740 745 750

Gln Gly Phe Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser
755 760 765

Ser Leu Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg
770 775 780

Asn Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg
785 790 795 800

Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp Asp

805

810

815

Thr Phe Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val Pro Lys Arg
820 825 830

Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln Pro Leu Asn
835 840 845

Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro His Ser Thr Ala
850 855 860

Val Gly Asn Pro Glu Tyr Leu Asn Thr Val Gln Pro Thr Cys Val Asn
865 870 875 880

Ser Thr Phe Asp Ser Pro Ala His Trp Ala Gln Lys Gly Ser His Gln
885 890 895

Ile Ser Leu Asp Asn Pro Asp Tyr Gln Gln Asp Phe Phe Pro Lys Glu
900 905 910

Ala Lys Pro Asn Gly Ile Phe Lys Gly Ser Thr Ala Glu Asn Ala Glu
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Tyr Leu Arg Val Ala Pro Gln Ser Ser Glu Phe Ile Gly Ala
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gct ctc tgc gcc gca ggt ggg gct ttg gag gaa aag aaa gtc tgc caa			96
Ala Leu Cys Ala Ala Gly Gly Ala Leu Glu Glu Lys Lys Val Cys Gln			
20	25	30	
ggc aca agt aac agg ctc acc caa ctg ggc act ttt gaa gac cac ttt			144
Gly Thr Ser Asn Arg Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe			
35	40	45	
ctg agc ctg cag agg atg tac aac aac tgt gaa gtg gtc ctt ggg aac			192
Leu Ser Leu Gln Arg Met Tyr Asn Asn Cys Glu Val Val Leu Gly Asn			
50	55	60	
ttg gaa att acc tat gtg caa agg aat tac gac ctt tcc ttc tta aag			240
Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys			
65	70	75	80
acc atc cag gag gtg gcc ggc tat gtc ctc att gcc ctc aac acc gtg			288
Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val			
85	90	95	
gag aga atc cct ttg gag aac ctg cag atc atc agg gga aat gct ctt			336
Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Ala Leu			
100	105	110	
tat gaa aac acc tat gcc tta gcc atc ctg tcc aac tat ggg aca aac			384
Tyr Glu Asn Thr Tyr Ala Leu Ala Ile Leu Ser Asn Tyr Gly Thr Asn			
115	120	125	
aga act ggg ctt agg gaa ctg ccc atg cgg aac tta cag gaa atc ctg			432
Arg Thr Gly Leu Arg Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu			
130	135	140	
att ggt gct gtg cga ttc agc aac aac ccc atc ctc tgc aat atg gat			480
Ile Gly Ala Val Arg Phe Ser Asn Asn Pro Ile Leu Cys Asn Met Asp			
145	150	155	160
act atc cag tgg agg gac atc gtc caa aac gtc ttt atg agc aac atg			528
Thr Ile Gln Trp Arg Asp Ile Val Gln Asn Val Phe Met Ser Asn Met			
165	170	175	
tca atg gac tta cag agc cat ccg agc agt tgc ccc aaa tgt gat cca			576
Ser Met Asp Leu Gln Ser His Pro Ser Ser Cys Pro Lys Cys Asp Pro			
180	185	190	
agc tgt ccc aat gga agc tgc tgg gga gga gag gag aac tgc cag			624
Ser Cys Pro Asn Gly Ser Cys Trp Gly Gly Glu Glu Asn Cys Gln			
195	200	205	
aaa ttg acc aaa atc atc tgt gcc cag caa tgt tcc cat cgc tgt cgt			672
Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser His Arg Cys Arg			
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ggc agg tcc ccc agt gac tgc tgc cac aac caa tgt gct gcg ggg tgt			720
Gly Arg Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys			

225	230	235	240	
aca ggg ccc cga gag agt gac tgt ctg gtc tgc caa aag ttc caa gat Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Gln Lys Phe Gln Asp				768
245	250		255	
gag gcc aca tgc aaa gac acc tgc cca cca ctc atg ctg tac aac ccc Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro				816
260	265		270	
acc acc tat cag atg gat gtc aac cct gaa ggg aag tac agc ttt ggt Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly				864
275	280		285	
gcc acc tgt gtg aag aag tgc ccc cga aac tac gtg gtg aca gat cat Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His				912
290	295		300	
ggc tca tgt gtc cga gcc tgt ggg cct gac tac tac gaa gtg gaa gaa Gly Ser Cys Val Arg Ala Cys Gly Pro Asp Tyr Tyr Glu Val Glu Glu				960
305	310		315	
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325	330		335	
tgt aat ggc ata ggc att ggt gaa ttt aaa gac aca ctc tcc ata aat Cys Asn Gly Ile Gly Ile Glu Phe Lys Asp Thr Leu Ser Ile Asn				1056
340	345		350	
gct aca aac atc aaa cac ttc aaa tac tgc act gcc atc agc ggg gac Ala Thr Asn Ile Lys His Phe Lys Tyr Cys Thr Ala Ile Ser Gly Asp				1104
355	360		365	
cct cac atc ctg cca gtg gcc ttt aag ggg gat tct ttc acg cgc act Leu His Ile Leu Pro Val Ala Phe Lys Gly Asp Ser Phe Thr Arg Thr				1152
370	375		380	
cct cct cta gac cca cga gaa cta gaa att cta aaa acc gta aag gaa Pro Pro Leu Asp Pro Arg Glu Leu Glu Ile Leu Lys Thr Val Lys Glu				1200
385	390		395	
400				
ata aca ggc ttt ttg ctg att cag gct tgg cct gat aac tgg act gac Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Asp Asn Trp Thr Asp				1248
405	410		415	
ctc cat gct ttc gag aac cta gaa ata ata cgt ggc aga aca aag caa Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln				1296
420	425		430	
cat ggt cag ttt tct ttg gcg gtc gtt ggc ctg aac atc aca tca ctg His Gly Gln Phe Ser Leu Ala Val Val Gly Leu Asn Ile Thr Ser Leu				1344
435	440		445	
450	455		460	
455				
460				

gga aac cga aat ttg tgc tac gca aac aca ata aac tgg aaa aaa ctc Gly Asn Arg Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu 465 470 475 480	1440
ttc ggg aca ccc aat cag aaa acc aaa atc atg aac aac aga gct gag Phe Gly Thr Pro Asn Gln Lys Thr Lys Ile Met Asn Asn Arg Ala Glu 485 490 495	1488
aaa gac tgc aag gcc gtg aac cac gtc tgc aat cct tta tgc tcc tcg Lys Asp Cys Lys Ala Val Asn His Val Cys Asn Pro Leu Cys Ser Ser 500 505 510	1536
gaa ggc tgc tgg ggc cct gag ccc agg gac tgt gtc tcc tgc cag aat Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Gln Asn 515 520 525	1584
gtg agc aga ggc agg gag tgc gtg gag aaa tgc aac atc ctg gag ggg Val Ser Arg Gly Arg Glu Cys Val Glu Lys Cys Asn Ile Leu Glu Gly 530 535 540	1632
gaa cca agg gag ttt gtg gaa aat tct gaa tgc atc cag tgc cat cca Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro 545 550 555 560	1680
gaa tgt ctg ccc cag gcc atg aac atc acc tgt aca ggc agg ggg cca Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro 565 570 575	1728
gac aac tgc atc cag tgt gcc cac tac att gat ggc cca cac tgt gtc Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val 580 585 590	1776
aag acc tgc cca gct ggc atc atg gga gag aac aac act ctg gtc tgg Lys Thr Cys Pro Ala Gly Ile Met Gly Glu Asn Asn Thr Leu Val Trp 595 600 605	1824
aag tat gca gat gcc aat aat gtc tgc cac cta tgc cac gcc aac tgt Lys Tyr Ala Asp Ala Asn Asn Val Cys His Leu Cys His Ala Asn Cys 610 615 620	1872
acc tat gga tgt gct ggg cca ggt ctt caa gga tgt gaa gtg tgg cca Thr Tyr Gly Cys Ala Gly Pro Gly Leu Gln Gly Cys Glu Val Trp Pro 625 630 635 640	1920
tct ggg cca aag ata cca tct att gcc act ggg att gtg ggt ggc ctc Ser Gly Pro Lys Ile Pro Ser Ile Ala Thr Gly Ile Val Gly Gly Leu 645 650 655	1968
ctc ttc ata gtg gtg gcc ctt ggg att ggc cta ttc atg cga aga Leu Phe Ile Val Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg 660 665 670	2016
cgt cac att gtt cga aag cgt aca cta cgc cgc ctg ctt caa gag aga Arg His Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg 675 680 685	2064

gag ctc gtg gaa cct ctc aca ccc agc gga gaa gct cca aac caa gcc Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala 690 695 700	2112
cac ttg agg ata tta aag aca gaa ttc aaa aag atc aaa gtt ctg His Leu Arg Ile Leu Lys Glu Thr Phe Lys Lys Ile Lys Val Leu 705 710 715 720	2160
ggt tcg gga gca ttt ggc aca gtg tat aag ggt ctc tgg atc cca gaa Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu 725 730 735	2208
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aca tct cca aaa gcc aac aaa gaa atc ctt gac gaa gcc tat gtg atg Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met 755 760 765	2304
gct agt gtg gac aac cct cat gta tgc cgc ctc ctg ggc atc tgt ctg Ala Ser Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu 770 775 780	2352
acc tcc act gtc cag ctc att aca cag ctc atg ccc tac ggt tgc ctc Thr Ser Thr Val Gln Leu Ile Thr Gln Leu Met Pro Tyr Gly Cys Leu 785 790 795 800	2400
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cg ^g cgt ttg gtg cac cgt gac ttg gca gcc agg aat gta ctg gtg aag Arg Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys 835 840 845	2544
aca cca cag cat gtc aag atc aca gat ttt ggg ctg gcc aaa ctg ctt Thr Pro Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu 850 855 860	2592
ggt gct gaa gag aaa gaa tat cat gcc gag ggg ggc aaa gtg cct atc Gly Ala Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile 865 870 875 880	2640
aag tgg atg gct ttg gaa tca att tta cac cga att tat aca cac caa Lys Trp Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln 885 890 895	2688
agt gat gtc tgg agc tat ggt gtc act gtg tgg gaa ctg atg acc ttt Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe 900 905 910	2736
ggg tcc aag cct tat gat gga atc cca gca agt gac atc tca tcc atc	2784

Gly Ser Lys Pro Tyr Asp Gly Ile Pro Ala Ser Asp Ile Ser Ser Ile			
915	920	925	
ctc gag aaa gga gaa cgc ctt cca cag cca cct atc tgc acc atc gat			2832
Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp			
930	935	940	
gtc tac atg atc atg gtc aag tgc tgg atg ata gat gct gat agc cgc			2880
Val Tyr Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg			
945	950	955	960
cca aag ttc cga gag ttg att ctt gaa ttc tcc aaa atg gcc cga gac			2928
Pro Lys Phe Arg Glu Leu Ile Leu Glu Phe Ser Lys Met Ala Arg Asp			
965	970	975	
cca cag cgc tac ctt gtt atc cag ggg gat gaa aga atg cat ttg cca			2976
Pro Gln Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro			
980	985	990	
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Ser Pro Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp			
995	1000	1005	
atg gag gat gta gtt gat gct gat gag tat ctt acc cca cag caa			3069
Met Glu Asp Val Val Asp Ala Asp Glu Tyr Leu Thr Pro Gln Gln			
1010	1015	1020	
ggc ttc ttc aac agc ccg tcc acg tcg agg act ccc ctc ttg agt			3114
Gly Phe Phe Asn Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser			
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tct ctg agt gca act agc aac aat tcc act gtg gct tgc att aat			3159
Ser Leu Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asn			
1040	1045	1050	
aga aat ggg agc tgc cgt gtc aaa gaa gac gcc ttc ttg cag cgg			3204
Arg Asn Gly Ser Cys Arg Val Lys Glu Asp Ala Phe Leu Gln Arg			
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tac agc tcc gac ccc aca ggt gct gta aca gag gac aac ata gat			3249
Tyr Ser Ser Asp Pro Thr Gly Ala Val Thr Glu Asp Asn Ile Asp			
1070	1075	1080	
gac gca ttc ctc cct gta cct gaa tat gta aac caa tct gtt ccc			3294
Asp Ala Phe Leu Pro Val Pro Glu Tyr Val Asn Gln Ser Val Pro			
1085	1090	1095	
aag agg cca gca ggc tct gtg cag aac cct gtc tat cac aat cag			3339
Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln			
1100	1105	1110	
ccc ctg cat cca gct cct gga aga gac ctg cat tat caa aat ccc			3384
Pro Leu His Pro Ala Pro Gly Arg Asp Leu His Tyr Gln Asn Pro			
1115	1120	1125	
cac agc aat gca gtg ggc aac cct gag tat ctc aac act gcc cag			3429
His Ser Asn Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Ala Gln			

Gly Ser Lys Pro Tyr Asp Gly Ile Pro Ala Ser Asp Ile Ser Ser Ile			
915	920	925	
ctc gag aaa gga gaa cgc ctt cca cag cca cct atc tgc acc atc gat	2832		
Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp			
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gtc tac atg atc atg gtc aag tgc tgg atg ata gat gct gat agc cgc	2880		
Val Tyr Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg			
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cca aag ttc cga gag ttg att ctt gaa ttc tcc aaa atg gcc cga gac	2928		
Pro Lys Phe Arg Glu Leu Ile Leu Glu Phe Ser Lys Met Ala Arg Asp			
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995	1000	1005	
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Gly Phe Phe Asn Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser			
1025	1030	1035	
tct ctg agt gca act agc aac aat tcc act gtg gct tgc att aat	3159		
Ser Leu Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asn			
1040	1045	1050	
aga aat ggg agc tgc cgt gtc aaa gaa gac gcc ttc ttg cag cgg	3204		
Arg Asn Gly Ser Cys Arg Val Lys Glu Asp Ala Phe Leu Gln Arg			
1055	1060	1065	
tac agc tcc gac ccc aca ggt gct gta aca gag gac aac ata gat	3249		
Tyr Ser Ser Asp Pro Thr Gly Ala Val Thr Glu Asp Asn Ile Asp			
1070	1075	1080	
gac gca ttc ctc cct gta cct gaa tat gta aac caa tct gtt ccc	3294		
Asp Ala Phe Leu Pro Val Pro Glu Tyr Val Asn Gln Ser Val Pro			
1085	1090	1095	
aag agg cca gca ggc tct gtg cag aac cct gtc tat cac aat cag	3339		
Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln			
1100	1105	1110	
ccc ctg cat cca gct cct gga aga gac ctg cat tat caa aat ccc	3384		
Pro Leu His Pro Ala Pro Gly Arg Asp Leu His Tyr Gln Asn Pro			
1115	1120	1125	
cac agc aat gca gtg ggc aac cct gag tat ctc aac act gcc cag	3429		
His Ser Asn Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Ala Gln			

1130	1135	1140	
cct acc tgt ctc agt agt ggg	ttt aac agc cct gca	ctc tgg atc	3474
Pro Thr Cys Leu Ser Ser Gly	Phe Asn Ser Pro Ala	Leu Trp Ile	
1145	1150	1155	
cag aaa ggc agt cac caa atg	agc cta gac aac cct	gac tac cag	3519
Gln Lys Gly Ser His Gln Met	Ser Leu Asp Asn Pro	Asp Tyr Gln	
1160	1165	1170	
cag gac ttc ttc ccc aag gaa	acc aag cca aat ggc	ata ttt aag	3564
Gln Asp Phe Phe Pro Lys Glu	Thr Lys Pro Asn Gly	Ile Phe Lys	
1175	1180	1185	
ggc ccc aca gct gaa aat gca	gag tac cta cggt gtg	gca cct cca	3609
Gly Pro Thr Ala Glu Asn Ala	Glu Tyr Leu Arg Val	Ala Pro Pro	
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1205	1210		
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20	25	30	
 Gly Thr Ser Asn Arg Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe			
35	40	45	
 Leu Ser Leu Gln Arg Met Tyr Asn Asn Cys Glu Val Val Leu Gly Asn			
50	55	60	
 Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys			
65	70	75	80
 Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val			
85	90	95	

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Ala Leu
100 105 110

Tyr Glu Asn Thr Tyr Ala Leu Ala Ile Leu Ser Asn Tyr Gly Thr Asn
115 120 125

Arg Thr Gly Leu Arg Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

Ile Gly Ala Val Arg Phe Ser Asn Asn Pro Ile Leu Cys Asn Met Asp
145 150 155 160

Thr Ile Gln Trp Arg Asp Ile Val Gln Asn Val Phe Met Ser Asn Met
165 170 175

Ser Met Asp Leu Gln Ser His Pro Ser Ser Cys Pro Lys Cys Asp Pro
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Ser Cys Pro Asn Gly Ser Cys Trp Gly Gly Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser His Arg Cys Arg
210 215 220

Gly Arg Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Gln Lys Phe Gln Asp
245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Pro Asp Tyr Tyr Glu Val Glu Glu
305 310 315 320

Asp Gly Ile Arg Lys Cys Lys Cys Asp Gly Pro Cys Arg Lys Val
325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Thr Leu Ser Ile Asn
340 345 350

Ala Thr Asn Ile Lys His Phe Lys Tyr Cys Thr Ala Ile Ser Gly Asp
355 360 365

Leu His Ile Leu Pro Val Ala Phe Lys Gly Asp Ser Phe Thr Arg Thr
370 375 380

Pro Pro Leu Asp Pro Arg Glu Leu Glu Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Asp Asn Trp Thr Asp
405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Gly Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

Gly Asn Arg Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Pro Asn Gln Lys Thr Lys Ile Met Asn Asn Arg Ala Glu
485 490 495

Lys Asp Cys Lys Ala Val Asn His Val Cys Asn Pro Leu Cys Ser Ser
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Gln Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Glu Lys Cys Asn Ile Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Ile Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Asn Asn Val Cys His Leu Cys His Ala Asn Cys
610 615 620

Thr Tyr Gly Cys Ala Gly Pro Gly Leu Gln Gly Cys Glu Val Trp Pro
625 630 635 640

Ser Gly Pro Lys Ile Pro Ser Ile Ala Thr Gly Ile Val Gly Gly Leu
645 650 655

Leu Phe Ile Val Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg
660 665 670

Arg His Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg
675 680 685

Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala
690 695 700

His Leu Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu
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Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu
725 730 735

Gly Glu Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala
740 745 750

Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met
755 760 765

Ala Ser Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu

770 775 780

Thr Ser Thr Val Gln Leu Ile Thr Gln Leu Met Pro Tyr Gly Cys Leu
785 790 795 800

Leu Asp Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu
805 810 815

Leu Asn Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp
820 825 830

Arg Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys
835 840 845

Thr Pro Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu
850 855 860

Gly Ala Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile
865 870 875 880

Lys Trp Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln
885 890 895

Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe
900 905 910

Gly Ser Lys Pro Tyr Asp Gly Ile Pro Ala Ser Asp Ile Ser Ser Ile
915 920 925

Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp
930 935 940

Val Tyr Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg
945 950 955 960

Pro Lys Phe Arg Glu Leu Ile Leu Glu Phe Ser Lys Met Ala Arg Asp
965 970 975

Pro Gln Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro
980 985 990

Ser Pro Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp
995 1000 1005

Met Glu Asp Val Val Asp Ala Asp Glu Tyr Leu Thr Pro Gln Gln
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Gly Phe Phe Asn Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser
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Ser Leu Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asn
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Arg Asn Gly Ser Cys Arg Val Lys Glu Asp Ala Phe Leu Gln Arg
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Tyr Ser Ser Asp Pro Thr Gly Ala Val Thr Glu Asp Asn Ile Asp
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Asp Ala Phe Leu Pro Val Pro Glu Tyr Val Asn Gln Ser Val Pro
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Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln
1100 1105 1110

Pro Leu His Pro Ala Pro Gly Arg Asp Leu His Tyr Gln Asn Pro
1115 1120 1125

His Ser Asn Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Ala Gln
1130 1135 1140

Pro Thr Cys Leu Ser Ser Gly Phe Asn Ser Pro Ala Leu Trp Ile
1145 1150 1155

Gln Lys Gly Ser His Gln Met Ser Leu Asp Asn Pro Asp Tyr Gln
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Gln Asp Phe Phe Pro Lys Glu Thr Lys Pro Asn Gly Ile Phe Lys
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 <213> ♂; Éö (Mus musculus)

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Ala Leu Cys Ala Ala Gly Gly Ala Leu Glu Glu Lys Lys Val Cys Gln		
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Gly Thr Ser Asn Arg Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe		
35 40 45		
ctg agc ctg cag agg atg tac aac tgt gaa gtg gtc ctt ggg aac		192
Leu Ser Leu Gln Arg Met Tyr Asn Asn Cys Glu Val Val Leu Gly Asn		
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ttg gaa att acc tat gtg caa agg aat tac gac ctt tcc ttc tta aag		240
Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys		
65 70 75 80		
acc atc cag gag gtg gcc ggc tat gtc ctc att gcc ctc aac acc gtg		288
Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val		
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gag aga atc cct ttg gag aac ctg cag atc atc agg gga aat gct ctt		336
Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Ala Leu		
100 105 110		
tat gaa aac acc tat gcc tta gcc atc ctg tcc aac tat ggg aca aac		384
Tyr Glu Asn Thr Tyr Ala Leu Ala Ile Leu Ser Asn Tyr Gly Thr Asn		
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aga act ggg ctt agg gaa ctg ccc atg cggt aac tta cag gaa atc ctg		432
Arg Thr Gly Leu Arg Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu		
130 135 140		

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tca atg gac tta cag agc cat ccg agc agt tgc ccc aaa tgt gat cca Ser Met Asp Leu Gln Ser His Pro Ser Ser Cys Pro Lys Cys Asp Pro 180 185 190	576
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Thr	Tyr	Gly	Val	Met	Val	Pro	Glu	Met	Leu	Leu	Gln	Ser	Ile	Ile	Leu	
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<211> 643

<212> PRT

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<400> 16

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Glu	Arg	Ile	Pro	Leu	Glu	Asn	Leu	Gln	Ile	Ile	Arg	Gly	Asn	Ala	Leu	
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Ile Gly Ala Val Arg Phe Ser Asn Asn Pro Ile Leu Cys Asn Met Asp
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Thr Ile Gln Trp Arg Asp Ile Val Gln Asn Val Phe Met Ser Asn Met
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Ser Met Asp Leu Gln Ser His Pro Ser Ser Cys Pro Lys Cys Asp Pro
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Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser His Arg Cys Arg
210 215 220

Gly Arg Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Gln Lys Phe Gln Asp
245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
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Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
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Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
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Gly Ser Cys Val Arg Ala Cys Gly Pro Asp Tyr Tyr Glu Val Glu Glu
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Asp Gly Ile Arg Lys Cys Lys Cys Asp Gly Pro Cys Arg Lys Val
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Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Thr Leu Ser Ile Asn
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Leu His Ile Leu Pro Val Ala Phe Lys Gly Asp Ser Phe Thr Arg Thr
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Pro Pro Leu Asp Pro Arg Glu Leu Glu Ile Leu Lys Thr Val Lys Glu
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Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Asp Asn Trp Thr Asp
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Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Gly Leu Asn Ile Thr Ser Leu
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Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
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Gly Asn Arg Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
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Phe Gly Thr Pro Asn Gln Lys Thr Lys Ile Met Asn Asn Arg Ala Glu
485 490 495

Lys Asp Cys Lys Ala Val Asn His Val Cys Asn Pro Leu Cys Ser Ser
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Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Gln Asn
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Val Ser Arg Gly Arg Glu Cys Val Glu Lys Cys Asn Ile Leu Glu Gly
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Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Ile Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Asn Asn Val Cys His Leu Cys His Ala Asn Cys
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Thr Tyr Gly Val Met Val Pro Glu Met Leu Leu Gln Ser Ile Ile Leu
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Lys Pro Ile

<210> 17

<211> 1968

<212> DNA

<213> ♂; Éö (Mus musculus)

<220>

<221> CDS

<222> (1)..(1965)

<223>

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gcg ctc tgc gcc gca ggt ggg gcg ttg gag gaa aag aaa gtc tgc caa 96
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20 25 30

ggc aca agt aac agg ctc acc caa ctg ggc act ttt gaa gac cac ttt 144
Gly Thr Ser Asn Arg Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

ctg agc ctg cag agg atg tac aac aac tgt gaa gtg gtc ctt ggg aac 192
Leu Ser Leu Gln Arg Met Tyr Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

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acc atc cag gag gtg gcc ggc tat gtc ctc att gcc ctc aac acc gtg Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val 85 90 95	288
gag aga atc cct ttg gag aac ctg cag atc atc agg gga aat gct ctt Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Ala Leu 100 105 110	336
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act atc cag tgg agg gac atc gtc caa aac gtc ttt atg agc aac atg Thr Ile Gln Trp Arg Asp Ile Val Gln Asn Val Phe Met Ser Asn Met 165 170 175	528
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gaa cca agg gag ttt gtg gaa aat tct gaa tgc atc cag tgc cat cca															1680		
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545						550					555				560		
gaa tgt ctg ccc cag gcc atg aac atc acc tgt aca ggc agg ggg cca															1728		
Glu	Cys	Leu	Pro	Gln	Ala	Met	Asn	Ile	Thr	Cys	Thr	Gly	Arg	Gly	Pro		
565						570					575						
gac aac tgc atc cag tgt gcc cac tac att gat ggc cca cac tgt gtc															1776		
Asp	Asn	Cys	Ile	Gln	Cys	Ala	His	Tyr	Ile	Asp	Gly	Pro	His	Cys	Val		
580						585					590						
aag acc tgc cca gct ggc atc atg gga gag aac aac act ctg gtc tgg															1824		
Lys	Thr	Cys	Pro	Ala	Gly	Ile	Met	Gly	Glu	Asn	Asn	Thr	Leu	Val	Trp		
595						600					605						
aag tat gca gat gcc aat aat gtc tgc cac cta tgc cac gcc aac tgt															1872		
Lys	Tyr	Ala	Asp	Ala	Asn	Asn	Val	Cys	His	Leu	Cys	His	Ala	Asn	Cys		
610						615					620						
acc tat gga tgt gct ggg cca ggt ctt caa gga tgt gaa gtg tgg cca															1920		
Thr	Tyr	Gly	Cys	Ala	Gly	Pro	Gly	Leu	Gln	Gly	Cys	Glu	Val	Trp	Pro		
625						630					635				640		
tct ggg tac gtt caa tgg cag tgg atc tta aag acc ttt tgg atc taa															1968		
Ser	Gly	Tyr	Val	Gln	Trp	Gln	Trp	Ile	Leu	Lys	Thr	Phe	Trp	Ile			
645						650					655						

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<211> 655

<212> PRT

<213> Ð;Êó(Mus musculus)

<400> 18

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1						5				10			15			

Ala	Leu	Cys	Ala	Ala	Gly	Gly	Ala	Leu	Glu	Glu	Lys	Lys	Val	Cys	Gln	
													20	25	30	

Gly Thr Ser Asn Arg Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe

35

40

45

Leu Ser Leu Gln Arg Met Tyr Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65 70 75 80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Ala Leu
100 105 110

Tyr Glu Asn Thr Tyr Ala Leu Ala Ile Leu Ser Asn Tyr Gly Thr Asn
115 120 125

Arg Thr Gly Leu Arg Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

Ile Gly Ala Val Arg Phe Ser Asn Asn Pro Ile Leu Cys Asn Met Asp
145 150 155 160

Thr Ile Gln Trp Arg Asp Ile Val Gln Asn Val Phe Met Ser Asn Met
165 170 175

Ser Met Asp Leu Gln Ser His Pro Ser Ser Cys Pro Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Gly Glu Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser His Arg Cys Arg
210 215 220

Gly Arg Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Gln Lys Phe Gln Asp
245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Pro Asp Tyr Tyr Glu Val Glu Glu
 305 . . . 310 . . . 315 . . . 320

Asp Gly Ile Arg Lys Cys Lys Lys Cys Asp Gly Pro Cys Arg Lys Val
 325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Thr Leu Ser Ile Asn
 340 345 350

Ala Thr Asn Ile Lys His Phe Lys Tyr Cys Thr Ala Ile Ser Gly Asp
 355 360 365

Leu His Ile Leu Pro Val Ala Phe Lys Gly Asp Ser Phe Thr Arg Thr
370 375 380

Pro Pro Leu Asp Pro Arg Glu Leu Glu Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Asp Asn Trp Thr Asp
405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Gly Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
· 450 455 460

Gly Asn Arg Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Pro Asn Gln Lys Thr Lys Ile Met Asn Asn Arg Ala Glu
485 490 495

Lys Asp Cys Lys Ala Val Asn His Val Cys Asn Pro Leu Cys Ser Ser
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Gln Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Glu Lys Cys Asn Ile Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Ile Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Asn Asn Val Cys His Leu Cys His Ala Asn Cys
610 615 620

Thr Tyr Gly Cys Ala Gly Pro Gly Leu Gln Gly Cys Glu Val Trp Pro
625 630 635 640

Ser Gly Tyr Val Gln Trp Gln Trp Ile Leu Lys Thr Phe Trp Ile
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<210> 19

<211> 1962

<212> DNA

<213> 41

<220>

<221> CDS

<222> (1)..(1962)

<223>

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gtc ctg gtg cta ctg ctg ggc gtc gcg ctg tgt tcc gcc gtg gag				96
Val Leu Val Leu Leu Leu Gly Val Ala Leu Cys Ser Ala Val Glu				
20 25 30				
gag aag aaa gtt tgt caa ggg aca aat aac aag ttg acc cag ctg ggg				144
Glu Lys Lys Val Cys Gln Gly Thr Asn Asn Lys Leu Thr Gln Leu Gly				
35 40 45				
cac gtg gaa gac cat ttc acc agc ctg cag aga atg tac aac aac tgc				192
His Val Glu Asp His Phe Thr Ser Leu Gln Arg Met Tyr Asn Asn Cys				
50 55 60				
gaa gtg gta ctg agt aac ctg gag att acc tac gtg gag cat aat cgc				240
Glu Val Val Leu Ser Asn Leu Glu Ile Thr Tyr Val Glu His Asn Arg				
65 70 75 80				
gat ctc acc ttc ctt aag acc ata cag gag gtt gca ggc tat gtg ctc				288
Asp Leu Thr Phe Leu Lys Thr Ile Gln Glu Val Ala Gly Tyr Val Leu				
85 90 95				
att gcg ctt aac atg gtg gac gtc att ccc tta gaa aac ctc cag att				336
Ile Ala Leu Asn Met Val Asp Val Ile Pro Leu Glu Asn Leu Gln Ile				
100 105 110				
atc cga ggg aat gtg ctt tat gac aac tct ttt gcc ctg gca gtt tta				384
Ile Arg Gly Asn Val Leu Tyr Asp Asn Ser Phe Ala Leu Ala Val Leu				
115 120 125				
tcc aat tac cac atg aat aaa acc cag gga ctt cga gag ctg cca atg				432
Ser Asn Tyr His Met Asn Lys Thr Gln Gly Leu Arg Glu Leu Pro Met				
130 135 140				
aaa cgg cta tca gaa att ctc aat gga ggt gtt aaa atc agc aac aac				480
Lys Arg Leu Ser Glu Ile Leu Asn Gly Gly Val Lys Ile Ser Asn Asn				
145 150 155 160				
ccc aaa ctg tgc aac atg gac act gtt ctc tgg aat gac atc att gat				528
Pro Lys Leu Cys Asn Met Asp Thr Val Leu Trp Asn Asp Ile Ile Asp				
165 170 175				
aca agc agg aag cct ctc aca gta ctt gac ttt gca agc aat ctt tct				576
Thr Ser Arg Lys Pro Leu Thr Val Leu Asp Phe Ala Ser Asn Leu Ser				
180 185 190				
tct tgt cca aaa tgc cat ccg aac tgc aca gaa gac cac tgc tgg ggt				624
Ser Cys Pro Lys Cys His Pro Asn Cys Thr Glu Asp His Cys Trp Gly				
195 200 205				

gct ggt gaa cag aac tgc cag act tta aca aaa gtc atc tgt gcc cag		672
Ala Gly Glu Gln Asn Cys Gln Thr Leu Thr Lys Val Ile Cys Ala Gln		
210	215	220
caa tgc tct ggc cg ^g tgc aga gga aag gtg ccc agt gac tgc tgc cac		720
Gln Cys Ser Gly Arg Cys Arg Gly Lys Val Pro Ser Asp Cys Cys His		
225	230	235
240		
aat cag tgt gct gca ggg tgc aca gga cct cg ^g gag agt gac tgc ctg		768
Asn Gln Cys Ala Ala Gly Cys Thr Gly Pro Arg Glu Ser Asp Cys Leu		
245	250	255
gca tgc cgc aag ttt cg ^g gat gat gct acc tgc aag gac aca tgt ccc		816
Ala Cys Arg Lys Phe Arg Asp Asp Ala Thr Cys Lys Asp Thr Cys Pro		
260	265	270
cca ctg gtc ctc tat aac ccc acc acc tat caa atg gat gtc aac cct		864
Pro Leu Val Leu Tyr Asn Pro Thr Thr Tyr Gln Met Asp Val Asn Pro		
275	280	285
gag gga aaa tac agc ttt gga gcc act tgt gtg agg gaa tgt cca cac		912
Glu Gly Lys Tyr Ser Phe Gly Ala Thr Cys Val Arg Glu Cys Pro His		
290	295	300
aac tat gtg gtg aca gat cat ggc tcc tgc gtt cg ^c tcg tgt aat act		960
Asn Tyr Val Val Thr Asp His Gly Ser Cys Val Arg Ser Cys Asn Thr		
305	310	315
320		
gat act tac gaa gtg gaa gaa aat ggt gtt cg ^g aag tgt aaa aaa tgt		1008
Asp Thr Tyr Glu Val Glu Glu Asn Gly Val Arg Lys Cys Lys Lys Cys		
325	330	335
gat ggg cta tgt agc aaa gtg tgc aat ggc att gga ata ggt gaa ctt		1056
Asp Gly Leu Cys Ser Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Leu		
340	345	350
aaa ggg atc cta tcc ata aat gcc aca aac atc gac tcc ttc aaa aac		1104
Lys Gly Ile Leu Ser Ile Asn Ala Thr Asn Ile Asp Ser Phe Lys Asn		
355	360	365
tgt acg aag atc aat ggg gat gtc acg att ctt cct gtt gca ttt cta		1152
Cys Thr Lys Ile Asn Gly Asp Val Ser Ile Leu Pro Val Ala Phe Leu		
370	375	380
ggg gat gcc ttc aca aag aca cta ccc ctt gac cct aag aag ctg gat		1200
Gly Asp Ala Phe Thr Lys Thr Leu Pro Leu Asp Pro Lys Lys Leu Asp		
385	390	395
400		
gtc ttt aga aca gtc aaa gaa ata tca gga ttt ttg ttg att cag gcc		1248
Val Phe Arg Thr Val Lys Glu Ile Ser Gly Phe Leu Leu Ile Gln Ala		
405	410	415
tgg cct gat aat gct act gat ctc tat gct ttt gaa aat ctg gag att		1296
Trp Pro Asp Asn Ala Thr Asp Leu Tyr Ala Phe Glu Asn Leu Glu Ile		
420	425	430
atc cga ggc cga acc aag cag cac ggc cag tat tcc ctt qct qtt qtt		1344

Ile Arg Gly Arg Thr Lys Gln His Gly Gln Tyr Ser Leu Ala Val Val		
435	440	445
aac ttg aaa ata cag tcg ttg ggg ctg cgc tcc ctc aag gaa ata agt		1392
Asn Leu Lys Ile Gln Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser		
450	455	460
gat gga gac att gcc att atg aag aac aag aac ctc tgc tat gct gac		1440
Asp Gly Asp Ile Ala Ile Met Lys Asn Lys Asn Leu Cys Tyr Ala Asp		
465	470	475
acc atg aac tgg cgc agc ttg ttt gct act cag agt cag aaa aca aaa		1488
Thr Met Asn Trp Arg Ser Leu Phe Ala Thr Gln Ser Gln Lys Thr Lys		
485	490	495
att ata cag aac aga aat aaa aat gat tgt act gct gac agg cat gtg		1536
Ile Ile Gln Asn Arg Asn Lys Asn Asp Cys Thr Ala Asp Arg His Val		
500	505	510
tgt gac ccg ctg tgc tcg gac gtg ggc tgc tgg ggc cca ggg ccc ttc		1584
Cys Asp Pro Leu Cys Ser Asp Val Gly Cys Trp Gly Pro Gly Pro Phe		
515	520	525
cac tgc ttt tcc tgc agg ttt ttc agt cgc cag aag gag tgt gta aaa		1632
His Cys Phe Ser Cys Arg Phe Phe Ser Arg Gln Lys Glu Cys Val Lys		
530	535	540
cag tgc aac atc ctg caa ggg gag cca cgt gag ttt gaa aga gac tcc		1680
Gln Cys Asn Ile Leu Gln Gly Glu Pro Arg Glu Phe Glu Arg Asp Ser		
545	550	555
aaa tgc ctc ccc tgc cac tca gag tgt ctg gta cag aac tcc act gca		1728
Lys Cys Leu Pro Cys His Ser Glu Cys Leu Val Gln Asn Ser Thr Ala		
565	570	575
tac aac aca acc tgc tct gga ccg ggc cca gac cac tgc atg aag tgt		1776
Tyr Asn Thr Thr Cys Ser Gly Pro Gly Pro Asp His Cys Met Lys Cys		
580	585	590
gcc cat ttt ata gat ggt ccc cac tgt gtg aag gcc tgc ccc gct ggg		1824
Ala His Phe Ile Asp Gly Pro His Cys Val Lys Ala Cys Pro Ala Gly		
595	600	605
gtc ctg ggt gag aat gat acc ctg gtc tgg aag tat gca gat gcc aat		1872
Val Leu Gly Glu Asn Asp Thr Leu Val Trp Lys Tyr Ala Asp Ala Asn		
610	615	620
gct gtt tgc cag ctc tgc cat cca aac tgt aca cga ggg tgc aaa ggg		1920
Ala Val Cys Gln Leu Cys His Pro Asn Cys Thr Arg Gly Cys Lys Gly		
625	630	635
cca ggt ctt gaa gga tgt cca aat ggc tcc aaa act cca tct		1962
Pro Gly Leu Glu Gly Cys Pro Asn Gly Ser Lys Thr Pro Ser		
645	650	

<211> 654

<212> PRT

<213> 41

<400> 20

Met Gly Val Arg Ser Pro Leu Ser Ala Ser Gly Pro Arg Gly Ala Ala
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Val Leu Val Leu Leu Leu Gly Val Ala Leu Cys Ser Ala Val Glu
20 25 30

Glu Lys Lys Val Cys Gln Gly Thr Asn Asn Lys Leu Thr Gln Leu Gly
35 40 45

His Val Glu Asp His Phe Thr Ser Leu Gln Arg Met Tyr Asn Asn Cys
50 55 60

Glu Val Val Leu Ser Asn Leu Glu Ile Thr Tyr Val Glu His Asn Arg
65 70 75 80

Asp Leu Thr Phe Leu Lys Thr Ile Gln Glu Val Ala Gly Tyr Val Leu
85 90 95

Ile Ala Leu Asn Met Val Asp Val Ile Pro Leu Glu Asn Leu Gln Ile
100 105 110

Ile Arg Gly Asn Val Leu Tyr Asp Asn Ser Phe Ala Leu Ala Val Leu
115 120 125

Ser Asn Tyr His Met Asn Lys Thr Gln Gly Leu Arg Glu Leu Pro Met
130 135 140

Lys Arg Leu Ser Glu Ile Leu Asn Gly Gly Val Lys Ile Ser Asn Asn
145 150 155 160

Pro Lys Leu Cys Asn Met Asp Thr Val Leu Trp Asn Asp Ile Ile Asp
165 170 175

Thr Ser Arg Lys Pro Leu Thr Val Leu Asp Phe Ala Ser Asn Leu Ser
180 185 190

Ser Cys Pro Lys Cys His Pro Asn Cys Thr Glu Asp His Cys Trp Gly
195 200 205

Ala Gly Glu Gln Asn Cys Gln Thr Leu Thr Lys Val Ile Cys Ala Gln
210 215 220

Gln Cys Ser Gly Arg Cys Arg Gly Lys Val Pro Ser Asp Cys Cys His
225 230 235 240

Asn Gln Cys Ala Ala Gly Cys Thr Gly Pro Arg Glu Ser Asp Cys Leu
245 250 255

Ala Cys Arg Lys Phe Arg Asp Asp Ala Thr Cys Lys Asp Thr Cys Pro
260 265 270

Pro Leu Val Leu Tyr Asn Pro Thr Thr Tyr Gln Met Asp Val Asn Pro
275 280 285

Glu Gly Lys Tyr Ser Phe Gly Ala Thr Cys Val Arg Glu Cys Pro His
290 295 300

Asn Tyr Val Val Thr Asp His Gly Ser Cys Val Arg Ser Cys Asn Thr
305 310 315 320

Asp Thr Tyr Glu Val Glu Glu Asn Gly Val Arg Lys Cys Lys Lys Cys
325 330 335

Asp Gly Leu Cys Ser Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Leu
340 345 350

Lys Gly Ile Leu Ser Ile Asn Ala Thr Asn Ile Asp Ser Phe Lys Asn
355 360 365

Cys Thr Lys Ile Asn Gly Asp Val Ser Ile Leu Pro Val Ala Phe Leu
370 375 380

Gly Asp Ala Phe Thr Lys Thr Leu Pro Leu Asp Pro Lys Lys Leu Asp
385 390 395 400

Val Phe Arg Thr Val Lys Glu Ile Ser Gly Phe Leu Leu Ile Gln Ala
405 410 415

Trp Pro Asp Asn Ala Thr Asp Leu Tyr Ala Phe Glu Asn Leu Glu Ile
420 425 430

Ile Arg Gly Arg Thr Lys Gln His Gly Gln Tyr Ser Leu Ala Val Val
435 440 445

Asn Leu Lys Ile Gln Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser
450 455 460

Asp Gly Asp Ile Ala Ile Met Lys Asn Lys Asn Leu Cys Tyr Ala Asp
465 470 475 480

Thr Met Asn Trp Arg Ser Leu Phe Ala Thr Gln Ser Gln Lys Thr Lys
485 490 495

Ile Ile Gln Asn Arg Asn Lys Asn Asp Cys Thr Ala Asp Arg His Val
500 505 510

Cys Asp Pro Leu Cys Ser Asp Val Gly Cys Trp Gly Pro Gly Pro Phe
515 520 525

His Cys Phe Ser Cys Arg Phe Phe Ser Arg Gln Lys Glu Cys Val Lys
530 535 540

Gln Cys Asn Ile Leu Gln Gly Glu Pro Arg Glu Phe Glu Arg Asp Ser
545 550 555 560

Lys Cys Leu Pro Cys His Ser Glu Cys Leu Val Gln Asn Ser Thr Ala
565 570 575

Tyr Asn Thr Thr Cys Ser Gly Pro Gly Pro Asp His Cys Met Lys Cys
580 585 590

Ala His Phe Ile Asp Gly Pro His Cys Val Lys Ala Cys Pro Ala Gly
595 600 605

Val Leu Gly Glu Asn Asp Thr Leu Val Trp Lys Tyr Ala Asp Ala Asn
610 615 620

Ala Val Cys Gln Leu Cys His Pro Asn Cys Thr Arg Gly Cys Lys Gly
625 630 635 640

Pro Gly Leu Glu Gly Cys Pro Asn Gly Ser Lys Thr Pro Ser
645 650

<210> 21

<211> 4134

<212> DNA

<213> 'Ó-(Drosophila melanogaster)

<220>

<221> CDS

<222> (1)..(3630)

<223>

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agc agc tcc atc ttg tcg gtg ctg ctg atc ctc gcc tgc atg gca tcc 96
Ser Ser Ser Ile Leu Ser Val Leu Leu Ile Leu Ala Cys Met Ala Ser
20 25 30

atc acc aca agc tca tcg gtc agc aat gcc ggc tat gtg gat aat ggc 144
Ile Thr Ser Ser Val Ser Asn Ala Gly Tyr Val Asp Asn Gly
35 40 45

aat atg aaa gtc tgc atc ggc act aaa tct cgg ctc tcc gtg ccc tcc 192
Asn Met Lys Val Cys Ile Gly Thr Lys Ser Arg Leu Ser Val Pro Ser
50 55 60

aac aag gaa cat cat tac cga aac ctc aga gat cgg tac acg aac tgt 240
Asn Lys Glu His His Tyr Arg Asn Leu Arg Asp Arg Tyr Thr Asn Cys
65 70 75 80

acg tat gtg gat ggc aac ttg aaa ctg acc tgg cta ccc aac gag aat 288
Thr Tyr Val Asp Gly Asn Leu Lys Leu Thr Trp Leu Pro Asn Glu Asn
85 90 95

ttg gac ctc agc ttc cta gac aac ata cgg gag gtc acc ggc tat att 336
Leu Asp Leu Ser Phe Leu Asp Asn Ile Arg Glu Val Thr Gly Tyr Ile
100 105 110

ctg atc agt cat gtg gac gtt aag aaa gtg gtg ttt ccc aaa cta caa 384
Leu Ile Ser His Val Asp Val Lys Lys Val Val Phe Pro Lys Leu Gln
115 120 125

atc att cgc gga cgc acg ctg ttc agc tta tcc gtg gag gag gag aag Ile Ile Arg Gly Arg Thr Leu Phe Ser Leu Ser Val Glu Glu Glu Lys 130 135 140	432
tat gcc ttg ttc gtc act tat tcc aaa atg tac acg ctg gag att ccc Tyr Ala Leu Phe Val Thr Tyr Ser Lys Met Tyr Thr Leu Glu Ile Pro 145 150 155 160	480
gat cta cgc gat gtc tta aat ggc caa gtg ggc ttc cac aac aac tac Asp Leu Arg Asp Val Leu Asn Gly Gln Val Gly Phe His Asn Asn Tyr 165 170 175	528
aat ctc tgc cac atg cga acg atc cag tgg tcg gag att gta tcc aac Asn Leu Cys His Met Arg Thr Ile Gln Trp Ser Glu Ile Val Ser Asn 180 185 190	576
ggc acg gat gca tac tac aac tac gac ttt act gct ccg gag cgc gag Gly Thr Asp Ala Tyr Tyr Asn Tyr Asp Phe Thr Ala Pro Glu Arg Glu 195 200 205	624
tgt ccc aag tgc cac gag agc tgc acg cac gga tgt tgg ggc gag ggt Cys Pro Lys Cys His Glu Ser Cys Thr His Gly Cys Trp Gly Glu Gly 210 215 220	672
ccc aag aat tgc cag aag ttc agc aag ctc acc tgc tcg cca cag tgt Pro Lys Asn Cys Gln Lys Phe Ser Lys Leu Thr Cys Ser Pro Gln Cys 225 230 235 240	720
gcc gga ggt cgt tgc tat gga cca aag ccg ccg gag tgt tgt cac ctc Ala Gly Gly Arg Cys Tyr Gly Pro Lys Pro Arg Glu Cys Cys His Leu 245 250 255	768
ttc tgc gcc gga tgc act ggt ccc acg caa aag gat tgc atc gcc Phe Cys Ala Gly Gly Cys Thr Gly Pro Thr Gln Lys Asp Cys Ile Ala 260 265 270	816
tgc aag aac ttc ttc gac gag gca gta tca aag gag gaa tgc ccg ccc Cys Lys Asn Phe Asp Glu Ala Val Ser Lys Glu Glu Cys Pro Pro 275 280 285	864
atg cgc aag tac aat ccc acc acc tat gtt ctt gaa acg aat cct gag Met Arg Lys Tyr Asn Pro Thr Thr Tyr Val Leu Glu Thr Asn Pro Glu 290 295 300	912
gga aag tat gcc tat ggt gcc acc tgc gtc aag gag tgt ccc ggt cat Gly Lys Tyr Ala Tyr Gly Ala Thr Cys Val Lys Glu Cys Pro Gly His 305 310 315 320	960
ctg ttg cgg gat aat ggc gcc tgc gtg cgc agc tgt ccc cag gag aag Leu Leu Arg Asp Asn Gly Ala Cys Val Arg Ser Cys Pro Gln Asp Lys 325 330 335	1008
atg gac aag ggg ggc gag tgt gtg ccc tgc aat gga ccg tgc ccc aaa Met Asp Lys Gly Gly Glu Cys Val Pro Cys Asn Gly Pro Cys Pro Lys 340 345 350	1056
acc tgc ccg ggc gtt act gtc ctg cat gcc ggc aac att gac tcg ttc	1104

Thr Cys Pro Gly Val Thr Val Leu His Ala Gly Asn Ile Asp Ser Phe			
355	360	365	
cgg aat tgt acg gtg atc gat ggc aac att cgc att ttg gat cag acc			1152
Arg Asn Cys Thr Val Ile Asp Gly Asn Ile Arg Ile Leu Asp Gln Thr			
370	375	380	
ttc tcg ggc ttc cag gat gtc tat gcc aac tac acg atg gga cca cga			1200
Phe Ser Gly Phe Gln Asp Val Tyr Ala Asn Tyr Thr Met Gly Pro Arg			
385	390	395	400
tac ata ccg ctg gat ccc gag cga cgg gag gtg ttc tcc acg gtg aag			1248
Tyr Ile Pro Leu Asp Pro Glu Arg Arg Glu Val Phe Ser Thr Val Lys			
405	410	415	
gag atc acc ggg tat ctg aat atc gag gga acc cac ccg cag ttc cgg			1296
Glu Ile Thr Gly Tyr Leu Asn Ile Glu Gly Thr His Pro Gln Phe Arg			
420	425	430	
aat ctg tcg tac ttt cgc aat ctg gaa aca att cat ggc cgc cag ctg			1344
Asn Leu Ser Tyr Phe Arg Asn Leu Glu Thr Ile His Gly Arg Gln Leu			
435	440	445	
atg gag agc atg ttt gcc gct ttg gcg atc gtt aag tca tcc ctg tac			1392
Met Glu Ser Met Phe Ala Ala Leu Ala Ile Val Lys Ser Ser Leu Tyr			
450	455	460	
agc ctg gag atg cgc aat ctg aag cag att agt tcc ggc agt gtg gtc			1440
Ser Leu Glu Met Arg Asn Leu Lys Gln Ile Ser Ser Gly Ser Val Val			
465	470	475	480
atc cag cat aat aga gac ctc tgc tac gta agc aat atc cgt tgg ccg			1488
Ile Gln His Asn Arg Asp Leu Cys Tyr Val Ser Asn Ile Arg Trp Pro			
485	490	495	
gcc att cag aag gag ccc gaa cag aag gtg tgg gtc aac gag aat ctc			1536
Ala Ile Gln Lys Glu Pro Glu Gln Lys Val Trp Val Asn Glu Asn Leu			
500	505	510	
agg gcg gat cta tgc gag aaa aat gga acc att tgc tcg gat cag tgc			1584
Arg Ala Asp Leu Cys Glu Lys Asn Gly Thr Ile Cys Ser Asp Gln Cys			
515	520	525	
aac gag gac ggc tgc tgg gga gct ggc acg gat cag tgc ctt acc tgc			1632
Asn Glu Asp Gly Cys Trp Gly Ala Gly Thr Asp Gln Cys Leu Thr Cys			
530	535	540	
aag aac ttc aat ttc aat ggc acc tgc atc gcc gac tgt ggt tat ata			1680
Lys Asn Phe Asn Phe Asn Gly Thr Cys Ile Ala Asp Cys Gly Tyr Ile			
545	550	555	560
tcc aat gcc tac aag ttt gac aat aga acg tgc aag ata tgc cat cca			1728
Ser Asn Ala Tyr Lys Phe Asp Asn Arg Thr Cys Lys Ile Cys His Pro			
565	570	575	
gag tgc cgg act tgc aat gga gct gga gca gat cac tgc cag gag tgc			1776
Glu Cys Arg Thr Cys Asn Gly Ala Gly Ala Asp His Cys Gln Glu Cys			

580	585	590	
gtc cat gtg agg gac ggt cag cac tgt gtg tcc gag tgc ccg aag aac Val His Val Arg Asp Gly Gln His Cys Val Ser Glu Cys Pro Lys Asn			1824
595	600	605	
aag tac aac gat cgt ggt gtc tgc cga gag tgc cac gcc acc tgc gat Lys Tyr Asn Asp Arg Gly Val Cys Arg Glu Cys His Ala Thr Cys Asp			1872
610	615	620	
gga tgc act ggg ccc aag gac acc atc ggc att gga gcg tgt acg acg Gly Cys Thr Gly Pro Lys Asp Thr Ile Gly Ile Gly Ala Cys Thr Thr			1920
625	630	635	640
tgc aat ttg gcc att atc aac aat gac gcc aca gta aaa cgc tgc ctg Cys Asn Leu Ala Ile Ile Asn Asn Asp Ala Thr Val Lys Arg Cys Leu			1968
645	650	655	
ctg aag gac gac aag tgc ccc gat ggg tat ttc tgg gag tat gtg cat Leu Lys Asp Asp Lys Cys Pro Asp Gly Tyr Phe Trp Glu Tyr Val His			2016
660	665	670	
ccg caa gag cag gga tcg ctg aag cca ttg gcc ggc aga gca gtt tgc Pro Gln Glu Gln Gly Ser Leu Lys Pro Leu Ala Gly Arg Ala Val Cys			2064
675	680	685	
cga aag tgc cat ccc ctt tgc gag ctg tgc acg aac tac gga tac cat Arg Lys Cys His Pro Leu Cys Glu Leu Cys Thr Asn Tyr Gly Tyr His			2112
690	695	700	
gaa cag gtg tgc tcc aag tgc acc cac tac aag cga cgg gag cag tgc Glu Gln Val Cys Ser Lys Cys Thr His Tyr Lys Arg Arg Glu Gln Cys			2160
705	710	715	720
gag acc gag tgt ccg gcc gat cac tac acg gat gag gag cag cgc gag Glu Thr Glu Cys Pro Ala Asp His Tyr Thr Asp Glu Glu Gln Arg Glu			2208
725	730	735	
tgc ttc cag cgc cac ccg gaa tgc aat ggt tgc acg ggt ccg ggt gcc Cys Phe Gln Arg His Pro Glu Cys Asn Gly Cys Thr Gly Pro Gly Ala			2256
740	745	750	
gac gat tgc aag tct tgc cgc aac ttt aag ttg ttc gac gcg aat gag Asp Asp Cys Lys Ser Cys Arg Asn Phe Lys Leu Phe Asp Ala Asn Glu			2304
755	760	765	
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785	790	795	800
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805	810	815	

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Ile Cys Ile Leu Cys Val Val Thr Tyr Ile Cys Arg Gln Lys Gln Lys			
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Ala Lys Lys Glu Thr Val Lys Met Thr Met Ala Leu Ser Gly Cys Glu			
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Leu Arg Ile Val Lys Asp Ala Glu Leu Arg Lys Gly Gly Val Leu Gly			
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atg gga gcc ttt gga cga gtg tac aag ggc gtt tgg gtg ccg gag ggt		2736	
Met Gly Ala Phe Gly Arg Val Tyr Lys Gly Val Trp Val Pro Glu Gly			
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gag aac gtc aag att cca gtg gcc att aag gag ctg ctc aag tcc aca		2784	
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ggc gcc gag tca agc gaa gag ttc ctc cgc gaa gcc tac atc atg gcc		2832	
Gly Ala Glu Ser Ser Glu Glu Phe Leu Arg Glu Ala Tyr Ile Met Ala			
930	935	940	
tct gag gag cac gtt aat ctg ctg aag ctc ctg gcc gtg tgc atg tcc		2880	
Ser Glu Glu His Val Asn Leu Leu Lys Leu Leu Ala Val Cys Met Ser			
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tca caa atg atg cta atc acg caa ctg atg ccg ctt ggc tgc ctg ttg		2928	
Ser Gln Met Met Leu Ile Thr Gln Leu Met Pro Leu Gly Cys Leu Leu			
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gac tat gtg cga aat aac cgg gac aag atc ggc tct aag gct ctg ctc		2976	
Asp Tyr Val Arg Asn Asn Arg Asp Lys Ile Gly Ser Lys Ala Leu Leu			
980	985	990	
aac tgg agc acg caa atc gcc aag ggc atg tcg tat ctg gag gag aag		3024	
Asn Trp Ser Thr Gln Ile Ala Lys Gly Met Ser Tyr Leu Glu Glu Lys			
995	1000	1005	
cga ctg gtc cac aga gac ttg gct gcc cgc aat gtc ctg gtg cag		3069	
Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Gln			
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Thr Pro Ser Leu Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu			
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<211> 1210

<212> PRT

<213> *Drosophila melanogaster*

<400> 22

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Asn	Met	Lys	Val	Cys	Ile	Gly	Thr	Lys	Ser	Arg	Leu	Ser	Val	Pro	Ser
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Asn	Lys	Glu	His	His	Tyr	Arg	Asn	Leu	Arg	Asp	Arg	Tyr	Thr	Asn	Cys
					65			70		75		80			

Thr	Tyr	Val	Asp	Gly	Asn	Leu	Lys	Leu	Thr	Trp	Leu	Pro	Asn	Glu	Asn
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Leu	Asp	Leu	Ser	Phe	Leu	Asp	Asn	Ile	Arg	Glu	Val	Thr	Gly	Tyr	Ile
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Leu	Ile	Ser	His	Val	Asp	Val	Lys	Lys	Val	Val	Phe	Pro	Lys	Leu	Gln
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Ile	Ile	Arg	Gly	Arg	Thr	Leu	Phe	Ser	Leu	Ser	Val	Glu	Glu	Glu	Lys
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Tyr Ala Leu Phe Val Thr Tyr Ser Lys Met Tyr Thr Leu Glu Ile Pro

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Asn Leu Cys His Met Arg Thr Ile Gln Trp Ser Glu Ile Val Ser Asn			
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Gly Thr Asp Ala Tyr Tyr Asn Tyr Asp Phe Thr Ala Pro Glu Arg Glu			
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Cys Pro Lys Cys His Glu Ser Cys Thr His Gly Cys Trp Gly Glu Gly			
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Pro Lys Asn Cys Gln Lys Phe Ser Lys Leu Thr Cys Ser Pro Gln Cys			
225	230	235	240
Ala Gly Gly Arg Cys Tyr Gly Pro Lys Pro Arg Glu Cys Cys His Leu			
245	250	255	
Phe Cys Ala Gly Gly Cys Thr Gly Pro Thr Gln Lys Asp Cys Ile Ala			
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Cys Lys Asn Phe Phe Asp Glu Ala Val Ser Lys Glu Glu Cys Pro Pro			
275	280	285	
Met Arg Lys Tyr Asn Pro Thr Thr Tyr Val Leu Glu Thr Asn Pro Glu			
290	295	300	
Gly Lys Tyr Ala Tyr Gly Ala Thr Cys Val Lys Glu Cys Pro Gly His			
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Leu Leu Arg Asp Asn Gly Ala Cys Val Arg Ser Cys Pro Gln Asp Lys			
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Met Asp Lys Gly Gly Glu Cys Val Pro Cys Asn Gly Pro Cys Pro Lys			
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Arg Asn Cys Thr Val Ile Asp Gly Asn Ile Arg Ile Leu Asp Gln Thr			
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Tyr Ile Pro Leu Asp Pro Glu Arg Arg Glu Val Phe Ser Thr Val Lys
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Asn Leu Ser Tyr Phe Arg Asn Leu Glu Thr Ile His Gly Arg Gln Leu
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Met Glu Ser Met Phe Ala Ala Leu Ala Ile Val Lys Ser Ser Leu Tyr
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Ile Gln His Asn Arg Asp Leu Cys Tyr Val Ser Asn Ile Arg Trp Pro
485 490 495

Ala Ile Gln Lys Glu Pro Glu Gln Lys Val Trp Val Asn Glu Asn Leu
500 505 510

Arg Ala Asp Leu Cys Glu Lys Asn Gly Thr Ile Cys Ser Asp Gln Cys
515 520 525

Asn Glu Asp Gly Cys Trp Gly Ala Gly Thr Asp Gln Cys Leu Thr Cys
530 535 540

Lys Asn Phe Asn Phe Asn Gly Thr Cys Ile Ala Asp Cys Gly Tyr Ile
545 550 555 560

Ser Asn Ala Tyr Lys Phe Asp Asn Arg Thr Cys Lys Ile Cys His Pro
565 570 575

Glu Cys Arg Thr Cys Asn Gly Ala Gly Ala Asp His Cys Gln Glu Cys
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Val His Val Arg Asp Gly Gln His Cys Val Ser Glu Cys Pro Lys Asn
595 600 605

Lys Tyr Asn Asp Arg Gly Val Cys Arg Glu Cys His Ala Thr Cys Asp
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Gly Cys Thr Gly Pro Lys Asp Thr Ile Gly Ile Gly Ala Cys Thr Thr
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Cys Asn Leu Ala Ile Ile Asn Asn Asp Ala Thr Val Lys Arg Cys Leu
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Leu Lys Asp Asp Lys Cys Pro Asp Gly Tyr Phe Trp Glu Tyr Val His
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Pro Gln Glu Gln Gly Ser Leu Lys Pro Leu Ala Gly Arg Ala Val Cys
675 680 685

Arg Lys Cys His Pro Leu Cys Glu Leu Cys Thr Asn Tyr Gly Tyr His
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Glu Gln Val Cys Ser Lys Cys Thr His Tyr Lys Arg Arg Glu Gln Cys
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Glu Thr Glu Cys Pro Ala Asp His Tyr Thr Asp Glu Glu Gln Arg Glu
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Cys Phe Gln Arg His Pro Glu Cys Asn Gly Cys Thr Gly Pro Gly Ala
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Asp Asp Cys Lys Ser Cys Arg Asn Phe Lys Leu Phe Asp Ala Asn Glu
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Thr Gly Pro Tyr Val Asn Ser Thr Met Phe Asn Cys Thr Ser Lys Cys
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Pro Leu Glu Met Arg His Val Asn Tyr Gln Tyr Thr Ala Ile Gly Pro
785 790 795 800

Tyr Cys Ala Ala Ser Pro Pro Arg Ser Ser Lys Ile Thr Ala Asn Leu
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850 855 860

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865 870 875 880

Leu Arg Ile Val Lys Asp Ala Glu Leu Arg Lys Gly Gly Val Leu Gly
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Met Gly Ala Phe Gly Arg Val Tyr Lys Gly Val Trp Val Pro Glu Gly
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Glu Asn Val Lys Ile Pro Val Ala Ile Lys Glu Leu Leu Lys Ser Thr
915 920 925

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Ser Glu Glu His Val Asn Leu Leu Lys Leu Leu Ala Val Cys Met Ser
945 950 955 960

Ser Gln Met Met Leu Ile Thr Gln Leu Met Pro Leu Gly Cys Leu Leu
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995 1000 1005

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His Leu Asp Ala Ala Met Arg Pro Thr Phe Lys Gln Leu Thr Thr
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Val Phe Ala Glu Phe Ala Arg Asp Pro Gly Arg Tyr Leu Ala Ile
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Pro Gly Asp Lys Phe Thr Arg Leu Pro Ala Tyr Thr Ser Gln Asp
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<212> DNA

<213> *Drosophila melanogaster*

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<212> DNA

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<220>

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Leu	Leu	Leu	Ala	His	Cys	Ile	Cys	Ile	Trp	Pro	Ala	Ser	Ala	Ala	Arg	
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cgc gat cgg gat cga gat cga ttc cta tac cgc agc agt tcg gcc caa Arg Asp Arg Asp Arg Asp Phe Leu Tyr Arg Ser Ser Ser Ala Gln	50	55	60	192
aat cga cag agg ggc ggg gcc aac ttc gcc ctg gga ctg gga gcc aac Asn Arg Gln Arg Gly Gly Ala Asn Phe Ala Leu Gly Leu Gly Ala Asn	65	70	75	240
gga gtc acc att ccc acc agt ctg gag gat aag aac aag aac gag ttc Gly Val Thr Ile Pro Thr Ser Leu Glu Asp Lys Asn Lys Asn Glu Phe	85	90	95	288
gtc aag ggg aaa atc tgc atc ggc act aaa tct cgg ctc tcc gtg ccc Val Lys Gly Lys Ile Cys Ile Gly Thr Lys Ser Arg Leu Ser Val Pro	100	105	110	336
tcc aac aag gaa cat cat tac cga aac ctc aga gat cgg tac acg aac Ser Asn Lys Glu His His Tyr Arg Asn Leu Arg Asp Arg Tyr Thr Asn	115	120	125	384
tgt acg tat gtg gat ggc aac ttg aaa ctg acc tgg cta ccc aac gag Cys Thr Val Asp Gly Asn Leu Lys Leu Thr Trp Leu Pro Asn Glu	130	135	140	432
aat ttg gac ctc agc ttc cta gac aac ata cgg gag gtc acc ggc tat Asn Leu Asp Leu Ser Phe Leu Asp Asn Ile Arg Glu Val Thr Gly Tyr	145	150	155	480
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ccc gat cta cgc gat gtc tta aat ggc caa gtg ggc ttc cac aac aac Pro Asp Leu Arg Asp Val Leu Asn Gly Gln Val Gly Phe His Asn Asn	210	215	220	672
tac aat ctc tgc cac atg cga acg atc cag tgg tcg gag att gta tcc Tyr Asn Leu Cys His Met Arg Thr Ile Gln Trp Ser Glu Ile Val Ser	225	230	235	720
aac ggc acg gat gca tac tac aac tac gac ttt act gct ccg gag cgc Asn Gly Thr Asp Ala Tyr Tyr Asn Tyr Asp Phe Thr Ala Pro Glu Arg	245	250	255	768
gag tgt ccc aag tgc cac gag agc tgc acg cac gga tgt tgg ggc gag				816

Glu	Cys	Pro	Lys	Cys	His	Glu	Ser	Cys	Thr	His	Gly	Cys	Trp	Gly	Glu	
260						265								270		
ggt	ccc	aag	aat	tgc	cag	aag	ttc	agc	aag	ctc	acc	tgc	tcg	cca	cag	864
Gly	Pro	Lys	Asn	Cys	Gln	Lys	Phe	Ser	Lys	Leu	Thr	Cys	Ser	Pro	Gln	
275							280							285		
tgt	gcc	gga	ggt	cgt	tgc	tat	gga	cca	aag	ccg	cg	gag	tgt	tgt	cac	912
Cys	Ala	Gly	Gly	Arg	Cys	Tyr	Gly	Pro	Lys	Pro	Arg	Glu	Cys	Cys	His	
290						295								300		
ctc	ttc	tgc	gcc	gga	gga	tgc	act	ggt	ccc	acg	caa	aag	gat	tgc	atc	960
Leu	Phe	Cys	Ala	Gly	Gly	Cys	Thr	Gly	Pro	Thr	Gln	Lys	Asp	Cys	Ile	
305							310				315			320		
gcc	tgc	aag	aac	ttc	ttc	gac	gag	gca	gta	tca	aag	gag	gaa	tgc	ccg	1008
Ala	Cys	Lys	Asn	Phe	Phe	Asp	Glu	Ala	Val	Ser	Lys	Glu	Glu	Cys	Pro	
325							330							335		
ccc	atg	cgc	aag	tac	aat	ccc	acc	acc	tat	gtt	ctt	gaa	acg	aat	cct	1056
Pro	Met	Arg	Lys	Tyr	Asn	Pro	Thr	Thr	Tyr	Val	Leu	Glu	Thr	Asn	Pro	
340						345								350		
gag	gga	aag	aat	tat	gcc	tat	ggt	gcc	acc	tgc	gtc	aag	gag	tgt	ccc	994
Glu	Gly	Lys	Tyr	Ala	Tyr	Gly	Ala	Thr	Cys	Val	Lys	Glu	Cys	Pro	Gly	
355						360								365		
cat	ctg	ttg	cg	gat	aat	ggc	gcc	tgc	gtg	cgc	agc	tgt	ccc	cag	gac	1152
His	Leu	Leu	Arg	Asp	Asn	Gly	Ala	Cys	Val	Arg	Ser	Cys	Pro	Gln	Asp	
370						375								380		
aag	atg	gac	aag	ggg	ggc	gag	tgt	gtg	ccc	tgc	aat	gga	ccg	tgc	ccc	1200
Lys	Met	Asp	Lys	Gly	Gly	Glu	Cys	Val	Pro	Cys	Asn	Gly	Pro	Cys	Pro	
385						390								400		
aaa	acc	tgc	ccg	ggc	gtt	act	gtc	ctg	cat	gcc	ggc	aac	att	gac	tgc	1248
Lys	Thr	Cys	Pro	Gly	Val	Thr	Val	Leu	His	Ala	Gly	Asn	Ile	Asp	Ser	
405						410								415		
ttc	cg	aat	tgt	acg	gt	atc	gat	ggc	aac	att	cgc	att	ttg	gat	cag	1296
Phe	Arg	Asn	Cys	Thr	Val	Ile	Asp	Gly	Asn	Ile	Arg	Ile	Leu	Asp	Gln	
420						425								430		
acc	ttc	tcg	ggc	ttc	cag	gat	gtc	tat	gcc	aac	tac	acg	atg	gga	cca	1344
Thr	Phe	Ser	Gly	Phe	Gln	Asp	Val	Tyr	Ala	Asn	Tyr	Thr	Met	Gly	Pro	
435						440								445		
cga	tac	ata	ccg	ctg	gat	ccc	gag	cga	cg	gag	gt	ttc	tcc	acg	gt	1392
Arg	Tyr	Ile	Pro	Leu	Asp	Pro	Glu	Arg	Arg	Glu	Val	Phe	Ser	Thr	Val	
450						455								460		
aag	gag	atc	acc	ggg	tat	ctg	aat	atc	gag	gga	acc	cac	ccg	cag	ttc	1440
Lys	Glu	Ile	Thr	Gly	Tyr	Leu	Asn	Ile	Glu	Gly	Thr	His	Pro	Gln	Phe	
465						470								475		
cgg	aat	ctg	tcg	tac	ttt	cgc	aat	ctg	gaa	aca	att	cat	ggc	cgc	cag	1488
Arg	Asn	Leu	Ser	Tyr	Phe	Arg	Asn	Leu	Glu	Thr	Ile	His	Gly	Arg	Gln	

485	490	495	
ctg atg gag agc atg ttt gcc gct ttg gcg atc gtt aag tca tcc ctg Leu Met Glu Ser Met Phe Ala Ala Leu Ala Ile Val Lys Ser Ser Leu 500	505	510	1536
tac agc ctg gag atg cgc aat ctg aag cag att agt tcc ggc agt gtg Tyr Ser Leu Glu Met Arg Asn Leu Lys Gln Ile Ser Ser Gly Ser Val 515	520	525	1584
gtc atc cag cat aat aga gac ctc tgc tac gta agc aat atc cgt tgg Val Ile Gln His Asn Arg Asp Leu Cys Tyr Val Ser Asn Ile Arg Trp 530	535	540	1632
ccg gcc att cag aag gag ccc gaa cag aag gtg tgg gtc aac gag aat Pro Ala Ile Gln Lys Glu Pro Glu Gln Lys Val Trp Val Asn Glu Asn 545	550	555	1680
ctc agg gcg gat cta tgc gag aaa aat gga acc att tgc tcg gat cag Leu Arg Ala Asp Leu Cys Glu Lys Asn Gly Thr Ile Cys Ser Asp Gln 565.	570	575	1728
tgc aac gag gac ggc tgc tgg gga gct ggc acg gat cag tgc ctt acc Cys Asn Glu Asp Gly Cys Trp Gly Ala Gly Thr Asp Gln Cys Leu Thr 580	585	590	1776
tgc aag aac ttc aat ttc aat ggc acc tgc atc gcc gac tgt ggt tat Cys Lys Asn Phe Asn Phe Asn Gly Thr Cys Ile Ala Asp Cys Gly Tyr 595	600	605	1824
ata tcc aat gcc tac aag ttt gac aat aga acg tgc aag ata tgc cat Ile Ser Asn Ala Tyr Lys Phe Asp Asn Arg Thr Cys Lys Ile Cys His 610	615	620	1872
cca gag tgc cgg act tgc aat gga gct gga gca gat cac tgc cag gag Pro Glu Cys Arg Thr Cys Asn Gly Ala Gly Ala Asp His Cys Gln Glu 625	630	635	1920
tgc gtc cat gtg agg gac ggt cag cac tgt gtg tcc gag tgc ccg aag Cys Val His Val Arg Asp Gly Gln His Cys Val Ser Glu Cys Pro Lys 645	650	655	1968
aac aag tac aac gat cgt ggt gtc tgc cga gag tgc cac gcc acc tgc Asn Lys Tyr Asn Asp Arg Gly Val Cys Arg Glu Cys His Ala Thr Cys 660	665	670	2016
gat gga tgc act ggg ccc aag gac acc atc ggc att gga gcg tgt acg Asp Gly Cys Thr Gly Pro Lys Asp Thr Ile Gly Ile Gly Ala Cys Thr 675	680	685	2064
acg tgc aat ttg gcc att atc aac aat gac gcc aca gta aaa cgc tgc Thr Cys Asn Leu Ala Ile Ile Asn Asn Asp Ala Thr Val Lys Arg Cys 690	695	700	2112
ctg ctg aag gac gac aag tgc ccc gat ggg tat ttc tgg gag tat gtg Leu Leu Lys Asp Asp Lys Cys Pro Asp Gly Tyr Phe Trp Glu Tyr Val 705	710	715	2160

cat ccg caa gag cag gga tcg ctg aag cca ttg gcc ggc aga gca gtt His Pro Gln Glu Gln Gly Ser Leu Lys Pro Leu Ala Gly Arg Ala Val	725 730 735	2208
tgc cga aag tgc cat ccc ctt tgc gag ctg tgc acg aac tac gga tac Cys Arg Lys Cys His Pro Leu Cys Glu Leu Cys Thr Asn Tyr Gly Tyr	740 745 750	2256
cat gaa cag gtg tgc tcc aag tgc acc cac tac aag cga cgg gag cag His Glu Gln Val Cys Ser Lys Cys Thr His Tyr Lys Arg Arg Glu Gln	755 760 765	2304
tgc gag acc gag tgt ccg gcc gat cac tac acg gat gag gag cag cgc Cys Glu Thr Glu Cys Pro Ala Asp His Tyr Thr Asp Glu Glu Gln Arg	770 775 780	2352
gag tgc ttc cag cgc cac ccg gaa tgc aat ggt tgc acg ggt ccg ggt Glu Cys Phe Gln Arg His Pro Glu Cys Asn Gly Cys Thr Gly Pro Gly	785 790 795 800	2400
gcc gac gat tgc aag tct tgc cgc aac ttt aag ttg ttc gac gcg aat Ala Asp Asp Cys Lys Ser Cys Arg Asn Phe Lys Leu Phe Asp Ala Asn	805 810 815	2448
gag acg ggt ccc tat gtg aac tcc acg atg ttc aat tgc acc tcg aag Glu Thr Gly Pro Tyr Val Asn Ser Thr Met Phe Asn Cys Thr Ser Lys	820 825 830	2496
tgt ccc ttg gag atg cga cat gtg aac tat cag tac acg gcc att gga Cys Pro Leu Glu Met Arg His Val Asn Tyr Gln Tyr Thr Ala Ile Gly	835 840 845	2544
ccc tac tgc gca gct agt ccg ccg agg agc agc aag ata act gcc aat Pro Tyr Cys Ala Ala Ser Pro Pro Arg Ser Ser Lys Ile Thr Ala Asn	850 855 860	2592
ctg gat gtg aac atg atc ttc att atc act ggt gct gtt ctg gtg ccg Leu Asp Val Asn Met Ile Phe Ile Ile Thr Gly Ala Val Leu Val Pro	865 870 875 880	2640
acg atc tgc atc ctc tgc gtg gtc aca tac att tgt cggcaa aagcaa Thr Ile Cys Ile Leu Cys Val Val Thr Tyr Ile Cys Arg Gln Lys Gln	885 890 895	2688
aag gcc aag aag gaa aca gtc aag atg acc atg gct ctg tct ggc tgc Lys Ala Lys Lys Glu Thr Val Lys Met Thr Met Ala Leu Ser Gly Cys	900 905 910	2736
gag gat tcc gag ccg ctg cgt ccc tcg aac att gga gcc aac cta tgc Glu Asp Ser Glu Pro Leu Arg Pro Ser Asn Ile Gly Ala Asn Leu Cys	915 920 925	2784
aag ttg cgc att gtc aag gac gcc gag ttg cgc aag ggc gga gtc ctt Lys Leu Arg Ile Val Lys Asp Ala Glu Leu Arg Lys Gly Gly Val Leu	930 935 940	2832

gga atg gga gcc ttt gga cga gtg tac aag ggc gtt tgg gtg ccg gag Gly Met Gly Ala Phe Gly Arg Val Tyr Lys Gly Val Trp Val Pro Glu 945 950 955 960	2880
ggt gag aac gtc aag att cca gtg gcc att aag gag ctg ctc aag tcc Gly Glu Asn Val Lys Ile Pro Val Ala Ile Lys Glu Leu Leu Lys Ser 965 970 975	2928
aca ggc gcc gag tca agc gaa gag ttc ctc cgc gaa gcc tac atc atg Thr Gly Ala Glu Ser Ser Glu Glu Phe Leu Arg Glu Ala Tyr Ile Met 980 985 990	2976
gcc tct gag gag cac gtt aat ctg ctg aag ctc ctg gcc gtg tgc atg Ala Ser Glu Glu His Val Asn Leu Leu Lys Leu Ala Val Cys Met 995 1000 1005	3024
tcc tca caa atg atg cta atc acg caa ctg atg ccg ctt ggc tgc Ser Ser Gln Met Met Leu Ile Thr Gln Leu Met Pro Leu Gly Cys 1010 1015 1020	3069
ctg ttg gac tat gtg cga aat aac cgg gac aag atc ggc tct aag Leu Leu Asp Tyr Val Arg Asn Asn Arg Asp Lys Ile Gly Ser Lys 1025 1030 1035	3114
gct ctg ctc aac tgg agc acg caa atc gcc aag ggc atg tcg tat Ala Leu Leu Asn Trp Ser Thr Gln Ile Ala Lys Gly Met Ser Tyr 1040 1045 1050	3159
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gtc ctg gtg cag act ccc tcg ctg gtg aag atc acc gac ttt ggg Val Leu Val Gln Thr Pro Ser Leu Val Lys Ile Thr Asp Phe Gly 1070 1075 1080	3249
ctg gcc aag ttg ctg agc agc gat tcc aat gag tac aag gct gct Leu Ala Lys Leu Leu Ser Ser Asp Ser Asn Glu Tyr Lys Ala Ala 1085 1090 1095	3294
ggc ggc aag atg ccc atc aag tgg ttg gca ctg gag tgc atc cgc Gly Gly Lys Met Pro Ile Lys Trp Leu Ala Leu Glu Cys Ile Arg 1100 1105 1110	3339
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acc att tgg gaa ctg ctg acc ttt ggc cag cgt cca cac gag aac Thr Ile Trp Glu Leu Leu Thr Phe Gly Gln Arg Pro His Glu Asn 1130 1135 1140	3429
atc cca gct aag gat att ccc gat ctt att gaa gtc ggt ctg aag Ile Pro Ala Lys Asp Ile Pro Asp Leu Ile Glu Val Gly Leu Lys 1145 1150 1155	3474
ctg gag cag ccg gag att tgt tcg ctg gac att tac tgt aca ctg	3519

Leu	Glu	Gln	Pro	Glu	Ile	Cys	Ser	Leu	Asp	Ile	Tyr	Cys	Thr	Leu	
1160							1165					1170			
ctc	tcg	tgc	tgg	cac	ttg	gat	gcc	gcc	atg	cgt	cca	acc	ttc	aag	3564
Leu	Ser	Cys	Trp	His	Leu	Asp	Ala	Ala	Met	Arg	Pro	Thr	Phe	Lys	
1175							1180					1185			
cag	ctg	act	acg	gtc	ttt	gct	gag	ttc	gcc	aga	gat	ccg	ggt	cgc	3609
Gln	Leu	Thr	Thr	Val	Phe	Ala	Glu	Phe	Ala	Arg	Asp	Pro	Gly	Arg	
1190							1195					1200			
tat	ctg	gcc	att	ccc	ggg	gataaggta	ccccgtgcc	ggcttacacg							3657
Tyr	Leu	Ala	Ile	Pro	Gly										
1205															
agtcaggatg	agaaggatct	catccgaaaa	ttggctccca	ccaccgatgg	gtccgaagcc										3717
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gactgcacgg	atgagatgcc	caagctgaac	cgctactgca	aggatcctag	taacaagaat										3837
tcgagtaccg	gagacgatga	gagggattcg	agtgcgggg	aagtggcgt	ggtaatctg										3897
cgctcgtatc	taccagtcga	tgaggatgtat	tatctgatgc	ccacttgcca	accgggtccc										3957
aacaacaaca	acaacatgaa	taatccaat	caaaacaata	tggcagctgt	ggcgtggct										4017
gccggctaca	tggatctcat	cgagtgccc	gttagtgtgg	acaatccgga	gtatctgcta										4077
aacgcgcaga	cactgggagt	tggggagtgc	ccgataacca	cccagaccat	cgggataaccg										4137
gtgatggag	gcccgccac	catggaggtc	aaggtgccaa	tgccaggcag	tgagccaacc										4197
agctccgtatc	acgagtaacta	caatgataacc	caacgggagt	tgcagccact	gcatcgaaac										4257
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<210> 25

<211> 1209

<212> PRT

<213> óÈó(Rattus norvegicus)

<400> 25

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Leu	Leu	Leu	Ala	His	Cys	Ile	Cys	Ile	Trp	Pro	Ala	Ser	Ala	Ala	Arg
								20				25			30

Asp Arg Tyr Ala Arg Gln Asn Asn Arg Gln Arg His Gln Asp Ile Asp
35 40 45

Arg Asp Arg Asp Arg Asp Arg Phe Leu Tyr Arg Ser Ser Ser Ala Gln
50 55 60

Asn Arg Gln Arg Gly Gly Ala Asn Phe Ala Leu Gly Leu Gly Ala Asn
65 70 75 80

Gly Val Thr Ile Pro Thr Ser Leu Glu Asp Lys Asn Lys Asn Glu Phe
85 90 95

Val Lys Gly Lys Ile Cys Ile Gly Thr Lys Ser Arg Leu Ser Val Pro
100 105 110

Ser Asn Lys Glu His His Tyr Arg Asn Leu Arg Asp Arg Tyr Thr Asn
115 120 125

Cys Thr Tyr Val Asp Gly Asn Leu Lys Leu Thr Trp Leu Pro Asn Glu
130 135 140

Asn Leu Asp Leu Ser Phe Leu Asp Asn Ile Arg Glu Val Thr Gly Tyr
145 150 155 160

Ile Leu Ile Ser His Val Asp Val Lys Lys Val Val Phe Pro Lys Leu
165 170 175

Gln Ile Ile Arg Gly Arg Thr Leu Phe Ser Leu Ser Val Glu Glu Glu
180 185 190

Lys Tyr Ala Leu Phe Val Thr Tyr Ser Lys Met Tyr Thr Leu Glu Ile
195 200 205

Pro Asp Leu Arg Asp Val Leu Asn Gly Gln Val Gly Phe His Asn Asn
210 215 220

Tyr Asn Leu Cys His Met Arg Thr Ile Gln Trp Ser Glu Ile Val Ser
225 230 235 240

Asn Gly Thr Asp Ala Tyr Tyr Asn Tyr Asp Phe Thr Ala Pro Glu Arg
245 250 255

Glu Cys Pro Lys Cys His Glu Ser Cys Thr His Gly Cys Trp Gly Glu
260 265 270

Gly Pro Lys Asn Cys Gln Lys Phe Ser Lys Leu Thr Cys Ser Pro Gln
275 280 285

Cys Ala Gly Gly Arg Cys Tyr Gly Pro Lys Pro Arg Glu Cys Cys His
290 295 300

Leu Phe Cys Ala Gly Gly Cys Thr Gly Pro Thr Gln Lys Asp Cys Ile
305 310 315 320

Ala Cys Lys Asn Phe Phe Asp Glu Ala Val Ser Lys Glu Glu Cys Pro
325 330 335

Pro Met Arg Lys Tyr Asn Pro Thr Thr Tyr Val Leu Glu Thr Asn Pro
340 345 350

Glu Gly Lys Tyr Ala Tyr Gly Ala Thr Cys Val Lys Glu Cys Pro Gly
355 360 365

His Leu Leu Arg Asp Asn Gly Ala Cys Val Arg Ser Cys Pro Gln Asp
370 375 380

Lys Met Asp Lys Gly Gly Glu Cys Val Pro Cys Asn Gly Pro Cys Pro
385 390 395 400

Lys Thr Cys Pro Gly Val Thr Val Leu His Ala Gly Asn Ile Asp Ser
405 410 415

Phe Arg Asn Cys Thr Val Ile Asp Gly Asn Ile Arg Ile Leu Asp Gln
420 425 430

Thr Phe Ser Gly Phe Gln Asp Val Tyr Ala Asn Tyr Thr Met Gly Pro
435 440 445

Arg Tyr Ile Pro Leu Asp Pro Glu Arg Arg Glu Val Phe Ser Thr Val
450 455 460

Lys Glu Ile Thr Gly Tyr Leu Asn Ile Glu Gly Thr His Pro Gln Phe
465 470 475 480

Arg Asn Leu Ser Tyr Phe Arg Asn Leu Glu Thr Ile His Gly Arg Gln

485

490

495

Leu Met Glu Ser Met Phe Ala Ala Leu Ala Ile Val Lys Ser Ser Leu
500 505 510

Tyr Ser Leu Glu Met Arg Asn Leu Lys Gln Ile Ser Ser Gly Ser Val
515 520 525

Val Ile Gln His Asn Arg Asp Leu Cys Tyr Val Ser Asn Ile Arg Trp
530 535 540

Pro Ala Ile Gln Lys Glu Pro Glu Gln Lys Val Trp Val Asn Glu Asn
545 550 555 560

Leu Arg Ala Asp Leu Cys Glu Lys Asn Gly Thr Ile Cys Ser Asp Gln
565 570 575

Cys Asn Glu Asp Gly Cys Trp Gly Ala Gly Thr Asp Gln Cys Leu Thr
580 585 590

Cys Lys Asn Phe Asn Phe Asn Gly Thr Cys Ile Ala Asp Cys Gly Tyr
595 600 605

Ile Ser Asn Ala Tyr Lys Phe Asp Asn Arg Thr Cys Lys Ile Cys His
610 615 620

Pro Glu Cys Arg Thr Cys Asn Gly Ala Gly Ala Asp His Cys Gln Glu
625 630 635 640

Cys Val His Val Arg Asp Gly Gln His Cys Val Ser Glu Cys Pro Lys
645 650 655

Asn Lys Tyr Asn Asp Arg Gly Val Cys Arg Glu Cys His Ala Thr Cys
660 665 670

Asp Gly Cys Thr Gly Pro Lys Asp Thr Ile Gly Ile Gly Ala Cys Thr
675 680 685

Thr Cys Asn Leu Ala Ile Ile Asn Asn Asp Ala Thr Val Lys Arg Cys
690 695 700

Leu Leu Lys Asp Asp Lys Cys Pro Asp Gly Tyr Phe Trp Glu Tyr Val
705 710 715 720

His Pro Gln Glu Gln Gly Ser Leu Lys Pro Leu Ala Gly Arg Ala Val
725 730 735

Cys Arg Lys Cys His Pro Leu Cys Glu Leu Cys Thr Asn Tyr Gly Tyr
740 745 750

His Glu Gln Val Cys Ser Lys Cys Thr His Tyr Lys Arg Arg Glu Gln
755 760 765

Cys Glu Thr Glu Cys Pro Ala Asp His Tyr Thr Asp Glu Glu Gln Arg
770 775 780

Glu Cys Phe Gln Arg His Pro Glu Cys Asn Gly Cys Thr Gly Pro Gly
785 790 795 800

Ala Asp Asp Cys Lys Ser Cys Arg Asn Phe Lys Leu Phe Asp Ala Asn
805 810 815

Glu Thr Gly Pro Tyr Val Asn Ser Thr Met Phe Asn Cys Thr Ser Lys
820 825 830

Cys Pro Leu Glu Met Arg His Val Asn Tyr Gln Tyr Thr Ala Ile Gly
835 840 845

Pro Tyr Cys Ala Ala Ser Pro Pro Arg Ser Ser Lys Ile Thr Ala Asn
850 855 860

Leu Asp Val Asn Met Ile Phe Ile Ile Thr Gly Ala Val Leu Val Pro
865 870 875 880

Thr Ile Cys Ile Leu Cys Val Val Thr Tyr Ile Cys Arg Gln Lys Gln
885 890 895

Lys Ala Lys Lys Glu Thr Val Lys Met Thr Met Ala Leu Ser Gly Cys
900 905 910

Glu Asp Ser Glu Pro Leu Arg Pro Ser Asn Ile Gly Ala Asn Leu Cys
915 920 925

Lys Leu Arg Ile Val Lys Asp Ala Glu Leu Arg Lys Gly Gly Val Leu
930 935 940

Gly Met Gly Ala Phe Gly Arg Val Tyr Lys Gly Val Trp Val Pro Glu
945 950 955 960

Gly Glu Asn Val Lys Ile Pro Val Ala Ile Lys Glu Leu Leu Lys Ser
965 970 975

Thr Gly Ala Glu Ser Ser Glu Glu Phe Leu Arg Glu Ala Tyr Ile Met
980 985 990

Ala Ser Glu Glu His Val Asn Leu Leu Lys Leu Leu Ala Val Cys Met
995 1000 1005

Ser Ser Gln Met Met Leu Ile Thr Gln Leu Met Pro Leu Gly Cys
1010 1015 1020

Leu Leu Asp Tyr Val Arg Asn Asn Arg Asp Lys Ile Gly Ser Lys
1025 1030 1035

Ala Leu Leu Asn Trp Ser Thr Gln Ile Ala Lys Gly Met Ser Tyr
1040 1045 1050

Leu Glu Glu Lys Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn
1055 1060 1065

Val Leu Val Gln Thr Pro Ser Leu Val Lys Ile Thr Asp Phe Gly
1070 1075 1080

Leu Ala Lys Leu Leu Ser Ser Asp Ser Asn Glu Tyr Lys Ala Ala
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Gly Gly Lys Met Pro Ile Lys Trp Leu Ala Leu Glu Cys Ile Arg
1100 1105 1110

Asn Arg Val Phe Thr Ser Lys Ser Asp Val Trp Ala Phe Gly Val
1115 1120 1125

Thr Ile Trp Glu Leu Leu Thr Phe Gly Gln Arg Pro His Glu Asn
1130 1135 1140

Ile Pro Ala Lys Asp Ile Pro Asp Leu Ile Glu Val Gly Leu Lys
1145 1150 1155

Leu Glu Gln Pro Glu Ile Cys Ser Leu Asp Ile Tyr Cys Thr Leu
1160 1165 1170

Leu Ser Cys Trp His Leu Asp Ala Ala Met Arg Pro Thr Phe Lys
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Tyr Leu Ala Ile Pro Gly
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<220>

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Gly Ser Phe Cys Ala Thr Pro Glu Lys Lys Val Cys Gln Gly Ala Asn
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aac aaa ctg act ctt ctg gga acg gtg gaa gac cat tat cag gtt ctg 144
Asn Lys Leu Thr Leu Leu Gly Thr Val Glu Asp His Tyr Gln Val Leu
35 40 45

ctc aga atg tac aga aac tgc act gtg gtt ctg gag aac ctg gaa att 192
Leu Arg Met Tyr Arg Asn Cys Thr Val Val Leu Glu Asn Leu Glu Ile
50 55 60

aca cat ata aca gag aaa tat gac ctg tcc ttc ctc aag aac atc cag 240
Thr His Ile Thr Glu Lys Tyr Asp Leu Ser Phe Leu Lys Ser Ile Gln
65 70 75 80

gaa gtt ggt ggc tat gtt ctt atc gcg gtc aat acg gtt tcc aaa atc Glu Val Gly Gly Tyr Val Leu Ile Ala Val Asn Thr Val Ser Lys Ile 85 90 95	288
cct ctg gag aac ctg cgc atc att cgc gga cac tca ctt tat gaa gac Pro Leu Glu Asn Leu Arg Ile Ile Arg Gly His Ser Leu Tyr Glu Asp 100 105 110	336
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gga gtc aag ttt tgc agg aac gat tat tta tgt aat gtg ggg acc atc Gly Val Lys Phe Cys Arg Asn Asp Tyr Leu Cys Asn Val Gly Thr Ile 145 150 155 160	480
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acg aaa gtg atc tgt gcg gag cag tgt tca ggg agg tgt aaa gga ccc Thr Lys Val Ile Cys Ala Glu Gln Cys Ser Gly Arg Cys Lys Gly Pro 210 215 220	672
aga ccc att gac tgc tgt aat gaa cac tgt gct gca tgc act gga Arg Pro Ile Asp Cys Cys Asn Glu His Cys Ala Ala Gly Cys Thr Gly 225 230 235 240	720
ccc aga cct aca gac tgt ctg gcc tgt aag gac ttc cag gat gaa ggg Pro Arg Pro Thr Asp Cys Leu Ala Cys Lys Asp Phe Gln Asp Glu Gly 245 250 255	768
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Cys Val Arg Thr Cys Ser Pro Gly Thr Tyr Glu Val Asp Glu Gly Gly			
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gtt cgc aaa tgt aag agg tgc gaa ggc ctg tgc cca aaa gtg tgc aat			1008
Val Arg Lys Cys Lys Arg Cys Glu Gly Leu Cys Pro Lys Val Cys Asn			
325	330	335	
ggg ttg gga atg ggg cct tta gcc aat gtc ctg tca atc aat gcc acc			1056
Gly Leu Gly Met Gly Pro Leu Ala Asn Val Leu Ser Ile Asn Ala Thr			
340	345	350	
aac atc gac tcc ttt gag aac tgc act aaa atc agc ggc aat gtt gcc			1104
Asn Ile Asp Ser Phe Glu Asn Cys Thr Lys Ile Ser Gly Asn Val Ala			
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atc ctc agc acc aca ttc aga ggt gac cca cat act aac act tca gga			1152
Ile Leu Ser Thr Thr Phe Arg Gly Asp Pro His Thr Asn Thr Ser Gly			
370	375	380	
ctg gat cca gca aag ctc agt gta ttg agt act gtc aaa gaa atc act			1200
Leu Asp Pro Ala Lys Leu Ser Val Leu Ser Thr Val Lys Glu Ile Thr			
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ggt tac ctg atg att cag ctg tgg ccg gag agc atg cag tcc ctt agt			1248
Gly Tyr Leu Met Ile Gln Leu Trp Pro Glu Ser Met Gln Ser Leu Ser			
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gcc ttc gaa aac ctt gag gtc atc cga gga cg ^g aca aaa aca caa gg ^a			1296
Ala Phe Glu Asn Leu Glu Val Ile Arg Gly Arg Thr Lys Thr Gln Gly			
420	425	430	
acg tac agc ttt gct gtc acc aag acg gcc atc act cat tta ggc atg			1344
Thr Tyr Ser Phe Ala Val Thr Lys Thr Ala Ile Thr His Leu Gly Met			
435	440	445	
cgt tct ctg agg gag atc agt gac ggg gac gtg tcc atc gtt aag aat			1392
Arg Ser Leu Arg Glu Ile Ser Asp Gly Asp Val Ser Ile Val Lys Asn			
450	455	460	
aag aat ctc tgc tac agc agc cct gaa cac tgg aaa cgc ctc ttc aag			1440
Lys Asn Leu Cys Tyr Ser Ser Pro Glu His Trp Lys Arg Leu Phe Lys			
465	470	475	480
tcc aaa caa cag tcg gtc aaa atg att gaa aat atg gat gct gcc acc			1488
Ser Lys Gln Gln Ser Val Lys Met Ile Glu Asn Met Asp Ala Ala Thr			
485	490	495	
tgc gcc aat cag aac agc aca tgt aat gag atg tgc acg gct gac ggc			1536
Cys Ala Asn Gln Asn Ser Thr Cys Asn Glu Met Cys Thr Ala Asp Gly			
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tgc tgg ggt ccc ggc ccc acc atg tgc ttc ggc tgt gag cat tac agc			1584
Cys Trp Gly Pro Gly Pro Thr Met Cys Phe Gly Cys Glu His Tyr Ser			
515	520	525	
cgc gga aaa cac tgc gtg gct tcc tgc aac ctg ctg aat ggt gag ccg			1632
Arg Gly Lys His Cys Val Ala Ser Cys Asn Leu Leu Asn Gly Glu Pro			

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ctg ctc atg aat gaa acc cag acc tgc aac ggc cct gga ccc gac aaa Leu Leu Met Asn Glu Thr Gln Thr Cys Asn Gly Pro Gly Pro Asp Lys 565 570 575			1728
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gct gac gtg aca cac gtt tgc cag ccc tgt cat gaa aac tgc acc cag Ala Asp Val Thr His Val Cys Gln Pro Cys His Glu Asn Cys Thr Gln 610 615 620			1872
gga tgt acg ggg cct gat cta aag gac tgc aaa gat ttc aaa agc tct Gly Cys Thr Gly Pro Asp Leu Lys Asp Cys Lys Asp Phe Lys Ser Ser 625 630 635 640			1920
ggg ttg ccg atg atc gct gct ggc gtt gtc gga ggt cta ctg gcg ttt Gly Leu Pro Met Ile Ala Ala Gly Val Val Gly Gly Leu Leu Ala Phe 645 650 655			1968
gtt att ctg gct ctt gga gtg gcc gtt ctc ctg cgc aga cgc cac atc Val Ile Leu Ala Leu Gly Val Ala Val Leu Leu Arg Arg Arg His Ile 660 665 670			2016
cgg agg aag agg act ctg aga cga ctc ctg caa gag aga gag ctt gtg Arg Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu Val 675 680 685			2064
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gag cat ccc cat gtg tgt cgt ctg ggc atc tgc ttg acc tcc aca Glu His Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr 770 775 780	2352
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tgc gtg cag atc gct aaa ggt atg aat tat cta gaa gag cgc cat ctt Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Glu Arg His Leu 820 825 830	2496
gtg cac cga gac ctg gca gca cgt aat gtg ttg gta aag acg cct cag Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro Gln 835 840 845	2544
cat gtc aag att acc gat ttc ggc ctc gcc aag ctg tta aac gcg gac His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Asn Ala Asp 850 855 860	2592
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Val Asp Ala Asp Glu Tyr Leu Val Pro Asn His Ser Phe Phe Ser	
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Asn Ser Ser Phe Gly Asn Cys Asn Ser Arg Asn Gly Asn Gly Tyr	
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Pro Ala Leu Asp Glu Thr Glu Glu Glu Tyr Leu Asn Cys Phe Lys	
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Ser Pro Ala Pro Ala Ser Val Val Glu Tyr Leu Asn Thr Ser His	
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Glu Val His	
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Leu Arg Met Tyr Arg Asn Cys Thr Val Val Leu Glu Asn Leu Glu Ile
50 55 60

Thr His Ile Thr Glu Lys Tyr Asp Leu Ser Phe Leu Lys Ser Ile Gln
65 70 75 80

Glu Val Gly Gly Tyr Val Leu Ile Ala Val Asn Thr Val Ser Lys Ile
85 90 95

Pro Leu Glu Asn Leu Arg Ile Ile Arg Gly His Ser Leu Tyr Glu Asp
100 105 110

Lys Phe Ala Leu Ala Val Leu Val Asn Phe Asn Asn Ser Ile Glu Gln
115 120 125

Gly Val Lys Glu Leu Pro Leu Thr Ser Leu Thr Glu Ile Leu Lys Gly
130 135 140

Gly Val Lys Phe Cys Arg Asn Asp Tyr Leu Cys Asn Val Gly Thr Ile
145 150 155 160

Glu Trp Ala Asp Ile Leu Asn Met Lys Ser Leu Pro Thr Ile Val Ser
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His Asn Ile Ser Tyr Gly Lys Asn Cys Gly Lys Cys Asp Pro Ser Cys

180 185 190

Phe Asn Gly Ser Cys Trp Gly Thr Gly Pro Asp Lys Cys Gln Arg Met
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Thr Lys Val Ile Cys Ala Glu Gln Cys Ser Gly Arg Cys Lys Gly Pro
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Arg Pro Ile Asp Cys Cys Asn Glu His Cys Ala Ala Gly Cys Thr Gly
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Pro Arg Pro Thr Asp Cys Leu Ala Cys Lys Asp Phe Gln Asp Glu Gly
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Thr Cys Lys Asp Ala Cys Pro Arg Leu Met Leu Tyr Asp Pro Asn Thr
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His Gln Leu Ala Pro Asn Pro Tyr Gly Lys Tyr Ser Phe Gly Ala Thr
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Cys Ile Lys Thr Cys Pro His Asn Tyr Val Val Thr Asp His Gly Ala
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Cys Val Arg Thr Cys Ser Pro Gly Thr Tyr Glu Val Asp Glu Gly Gly
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Val Arg Lys Cys Lys Arg Cys Glu Gly Leu Cys Pro Lys Val Cys Asn
325 330 335

Gly Leu Gly Met Gly Pro Leu Ala Asn Val Leu Ser Ile Asn Ala Thr
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Asn Ile Asp Ser Phe Glu Asn Cys Thr Lys Ile Ser Gly Asn Val Ala
355 360 365

Ile Leu Ser Thr Thr Phe Arg Gly Asp Pro His Thr Asn Thr Ser Gly
370 375 380

Leu Asp Pro Ala Lys Leu Ser Val Leu Ser Thr Val Lys Glu Ile Thr
385 390 395 400

Gly Tyr Leu Met Ile Gln Leu Trp Pro Glu Ser Met Gln Ser Leu Ser
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Ala Phe Glu Asn Leu Glu Val Ile Arg Gly Arg Thr Lys Thr Gln Gly
420 425 430

Thr Tyr Ser Phe Ala Val Thr Lys Thr Ala Ile Thr His Leu Gly Met
435 440 445

Arg Ser Leu Arg Glu Ile Ser Asp Gly Asp Val Ser Ile Val Lys Asn
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Lys Asn Leu Cys Tyr Ser Ser Pro Glu His Trp Lys Arg Leu Phe Lys
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Ser Lys Gln Gln Ser Val Lys Met Ile Glu Asn Met Asp Ala Ala Thr
485 490 495

Cys Ala Asn Gln Asn Ser Thr Cys Asn Glu Met Cys Thr Ala Asp Gly
500 505 510

Cys Trp Gly Pro Gly Pro Thr Met Cys Phe Gly Cys Glu His Tyr Ser
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Arg Gly Lys His Cys Val Ala Ser Cys Asn Leu Leu Asn Gly Glu Pro
530 535 540

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Leu Leu Met Asn Glu Thr Gln Thr Cys Asn Gly Pro Gly Pro Asp Lys
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Cys Thr Val Cys Ala Asn Tyr Lys Asp Gly Pro His Cys Val His Arg
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Cys Pro Gln Gly Val Pro Gly Glu Lys Asp Thr Leu Ile Trp Lys Tyr
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Gly Cys Thr Gly Pro Asp Leu Lys Asp Cys Lys Asp Phe Lys Ser Ser
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Gly Leu Pro Met Ile Ala Ala Gly Val Val Gly Gly Leu Leu Ala Phe
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Val Ile Leu Ala Leu Gly Val Ala Val Leu Leu Arg Arg Arg His Ile
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675 680 685

Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu Arg
690 695 700

Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser Gly
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Ala Phe Gly Thr Val His Lys Gly Leu Trp Val Pro Glu Gly Glu Asn
725 730 735

Val Lys Ile Pro Val Ala Ile Lys Val Leu Arg Glu Ala Thr Ser Pro
740 745 750

Lys Ala Asn Lys Glu Ile Met Asp Glu Ala Tyr Val Met Ala Ser Val
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Glu His Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr
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Val Gln Leu Ile Thr Gln Leu Met Pro Tyr Gly Cys Leu Leu Asp Tyr
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Val Arg Glu Asn Lys Asp Arg Ile Gly Ser Gln His Leu Leu Asn Trp
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Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Glu Arg His Leu
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850 855 860

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865 870 875 880

Ala Leu Glu Ser Ile Gln His Arg Thr Tyr Thr His Gln Ser Asp Val
885 890 895

Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Thr Lys
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Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ala Gly Val Leu Glu Lys
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Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met
930 935 940

Ile Met Val Lys Cys Trp Met Ile Asp Ala Glu Ser Arg Pro Arg Phe
945 950 955 960

Arg Glu Leu Ile Ala Glu Phe Thr Lys Met Ala Arg Asp Pro Ser Arg
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Tyr Leu Val Ile Gln Gly Asp Asp Arg Met His Leu Pro Ser Pro Ser
980 985 990

Asp Ser Lys Phe Tyr Arg Ser Leu Met Ser Gly Glu Leu Asp Glu Ala
995 1000 1005

Val Asp Ala Asp Glu Tyr Leu Val Pro Asn His Ser Phe Phe Ser
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Ser Pro Ser Thr Ser Arg Thr Gln Leu Leu His Ser Val Ser Leu
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Thr Glu Arg Phe Gln Glu Gly Asp Phe Gln Pro Ala Pro Gly Tyr
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1085

1090

1095

Tyr Gln Gln Pro His Gly Pro Pro Arg Thr Leu Leu His Ser Ser
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1115 1120 1125

Ser Pro Ala Pro Ala Ser Val Val Glu Tyr Leu Asn Thr Ser His
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Asp Tyr Gln Gln Asp Phe Cys Pro Leu Glu Leu Lys Thr His Thr
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Glu Val His
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